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R C van Dijk

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Anmelder/Applicant(s)/Demandeur(s):

Applied Research Systems ARS Holding N.V.
Pietermaai 15
Curacao
ANTILLES NEERLANDAISES

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Novel chemokine-like polypeptides

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NOVEL CHEMOKINE-LIKE POLYPEPTIDES

FIELD OF THE INVENTION

The present invention relates to nucleic acid sequences identified in human genome as encoding for novel polypeptides, more specifically for chemokine-like polypeptides.

BACKGROUND OF THE INVENTION

The mammalian immune response is based on a series of complex, network-like interactions involving cellular components (such as lymphocytes or granulocytes) and soluble proteins, capable of modulating cellular activities (movement, proliferation, differentiation, etc.). Thus, there is considerable interest in the isolation and characterization of cell modulating factors, with the purpose of providing significant advancements in the diagnosis, prevention, and therapy of human disorders, in particular the ones associated to the immune system.

Chemokines are amongst these soluble proteins, since they are involved in the directional migration and activation of cells. This superfamily of small (70-130 amino acids), secreted, heparin-binding, pro-inflammatory proteins is known especially for the role in the extravasation of leukocytes from the blood to tissue localizations needing the recruitment of these cells (Baggiolini M et al., 1997; Yoshie OF et al., 2001; Fernandez EJ and Lolis E, 2002).

Chemokines are not only functionally related but also structurally related; since they all contain a central region in which conserved Cysteines form intramolecular bonds. In particular, the number and the position of the conserved cysteines in the N-terminal sequence of the mature polypeptides is the basic criteria for the generally

recognized classification of chemokines, essentially divided between chemokines containing isolated or adjacent Cysteines , or Cysteines separated by 1-3 amino acids.

A series of membrane receptors, all heptahelical G-protein coupled receptors, are the binding partners that allow chemokines to exert their biological activity on the target cells. The physiological effects of chemokines result from a complex and integrated system of concurrent interactions. Different cells can present specific combinations of receptors according to their state and/or type. Moreover, chemokine receptors often have overlapping ligand specificity, so that a single receptor can bind different chemokines, as well a single chemokine can bind different receptors, still at high affinity.

Usually chemokines are produced at the site of an injury, inflammation, or other tissue alteration, and exert their activity in a paracrine or autocrine fashion. However, cell-type specific migration and activation in inflammatory and immune processes is not the sole activity of chemokines. Other physiological activities, such as hematopoiesis or angiogenesis, and pathological conditions, such as metastasis, transplant rejection, Alzehimer's disease or atherosclerosis, appear to be regulated by, at least, some of these proteins, since chemokine are found considerably up-regulated and/or activated in several animal models or clinical samples (Haskell CA et al., 2002; Lucas AD and Greaves DR, 2001; Frederick MJ and Clayman GL, 2001; Godessart N and Kunkel SL, 2001; Reape TJ and Groot PH, 1999).

There are potential drawbacks in using chemokines as therapeutic agents (tendency to aggregate and promiscuous binding, in particular), but molecules having antagonistic properties against chemokines are widely considered as offering valuable opportunities for therapeutic intervention in disorders associated to excessive chemokine activities. The inhibition of specific chemokines and their receptors is

considered a solution for preventing undesirable or uncontrolled cellular processes, such as recruitment or activation (Baggiolini M, 2001; Proudfoot A, 2000; Rossi DF and Zlotnik A, 2000).

The technologies and information on human genome and physiology now available (Quinn-Senger KE et al., 2002; Browne MJ, 2000) were also used for discovering novel chemokines and receptors possibly providing new and useful therapeutic molecules and targets. Initially, chemokines genes were regularly mapped on chromosomes 4 and 17, in gene-rich areas of human genome (Nomiyama H et al., 2001), but the literature provides many examples of different approaches for characterizing novel chemokines by making use of bioinformatics analysis of transcripts, which are expressed in lymphoid and other tissues with individually characteristic patterns and mapped to chromosomal loci different from the traditional chemokine gene clusters (WO 02/70706; Wells TN and Peitsch MC, 2000; Chantry DF et al., 1998 ; Rossi D et al., 1997).

Many novel chemokines have been already identified by applying strict homology criteria to known chemokines. However, since the actual content in polypeptide-encoding sequence in human genome for chemokines (and for any other protein family) is still unknown, the possibility still exists to identify DNA sequence encoding polypeptide having chemotactic activities by applying alternative and less strict homology/structural criteria to the totality of Open Reading Frames (ORFs, that is, genomic sequences containing consecutive triplets of nucleotides coding for amino acids, not interrupted by a termination codon and potentially translatable in a polypeptide) present in human genome.

SUMMARY OF THE INVENTION

The invention is based upon the identification of Open Reading Frames (ORFs) in human genome encoding novel chemokine-like polypeptides.

Accordingly, the invention provides isolated polypeptides having the amino acid sequence given by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, and their mature forms, variants, and fragments, as polypeptides having chemotactic activity. The invention includes also the nucleic acids encoding them, vectors containing such nucleic acids, and cell containing these vectors or nucleic acids, as well as other related reagents such as fusion proteins, ligands, and antagonists.

The invention provides methods for identifying and making these molecules, for preparing pharmaceutical compositions containing them, and for using them in the diagnosis, prevention and treatment of diseases.

DESCRIPTION OF THE FIGURES

Figure 1: alignment of the ORF contained in the DNA sequence GNSQ_1754 (SEQ ID NO: 1) with the protein sequence p1754 (SEQ ID NO: 2). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated with §. The arrows indicate the position of the primers CL_1754_5 (forward) and CL_1754_3 (reverse) in the ORF sequence.

Figure 2: alignment of the ORF contained in the DNA sequence GNSQ_0711 (SEQ ID NO: 3) with the protein sequence p0711 (SEQ ID NO: 4). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated

with §. The arrows indicate the position of the primers CL_0711_5 (forward) and CL_0711_3 (reverse) in the ORF sequence.

Figure 3: alignment of the ORF contained in the DNA sequence GNSQ_2882 (SEQ ID NO: 5) with the protein sequence p2882 (SEQ ID NO: 6). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated with §.

Figure 4: alignment of the ORF contained in the DNA sequence GNSQ_4711 (SEQ ID NO: 7) with the protein sequence p4711 (SEQ ID NO: 8). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated with §.

Figure 5: alignment of the ORF contained in the DNA sequence GNSQ_4320 (SEQ ID NO: 9) with the protein sequence p4320 (SEQ ID NO: 10). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated with §. The arrows indicate the position of the primers CL_4320_5 (forward) and CL_4320_3 (reverse) in the ORF sequence.

Figure 6: alignment of the ORF contained in the DNA sequence GNSQ_5008 (SEQ ID NO: 11) with the protein sequence p5008 (SEQ ID NO: 12). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated with §. The arrows indicate the position of the primers CL_5008_5 (forward) and CL_5008_3 (reverse) in the ORF sequence.

Figure 7: alignment of the ORF contained in the DNA sequence GNSQ_0210 (SEQ ID NO: 13) with the protein sequence p0210 (SEQ ID NO: 14). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated with §. The arrows indicate the position of the primers CL_0210_5 (forward) and CL_0210_3 (reverse) in the ORF sequence.

Figure 8: alignment of the ORF contained in the DNA sequence GNSQ_4922 (SEQ ID NO: 15) with the protein sequence p4922 (SEQ ID NO: 16). The predicted N-terminal signal sequence is boxed. The predicted C-terminal alpha helix is underlined. The codons matching the original selection criteria are indicated with §. The arrows indicate the position of the primers CL_4922_5 (forward) and CL_4922_3 (reverse) in the ORF sequence.

Figure 9: alignment of human CXCL chemokines with the CXC chemokine-like protein sequences of the invention p1754 (SEQ ID NO: 2), p0711 (SEQ ID NO: 4), p2882 (SEQ ID NO: 6), p0210 (SEQ ID NO: 14), and p4922 (SEQ ID NO: 16). The following human CXCL chemokines have been considered: CXCL1 (SWISSPROT Acc. N° P09341), CXCL2 (SWISSPROT Acc. N° P19875), CXCL3 (SWISSPROT Acc. N° NP_002081), CXCL4 (SWISSPROT Acc. N° NP_002610), CXCL5 (SWISSPROT Acc. N° P42830), CXCL6 (SWISSPROT Acc. N° P80162), CXCL7 (SWISSPROT Acc. N° P02775), CXCL8 (SWISSPROT Acc. N° P10145), CXCL9 (SWISSPROT Acc. N° Q07325), CXCL10 (SWISSPROT Acc. N° P02778), CXCL11 (SWISSPROT Acc. N° O14625). The protein sequences are arranged distinguishing three main regions: the N-terminal region (containing the signal sequence), the central Cys-rich region (the conserved Cysteines matching the original selection

criteria are indicated with §), and the C-terminal region (containing the alpha helix).

Figure 10: alignment of human CCL chemokines with the CXC chemokine-like protein sequences of the invention p4711 (SEQ ID NO: 8), p4320 (SEQ ID NO: 10), and GNSQ_5008 (SEQ ID NO: 12). The following human CCL chemokines have been considered: CCL1 (SWISSPROT Acc. N° P22362), CCL2 (SWISSPROT Acc. N° P13500), CCL3 (SWISSPROT Acc. N° P10147), CCL4 (SWISSPROT Acc. N° P13236), CCL5 (SWISSPROT Acc. N° P13501), CCL7 (SWISSPROT Acc. N° P80098), CCL8 (SWISSPROT Acc. N° P80075). The protein sequences are arranged distinguishing three main regions: the N-terminal region (containing the signal sequence), the central Cys-rich region (the conserved Cysteines matching the original selection criteria are indicated with §), and the C-terminal region (containing the alpha helix).

Figure 11: Map of the pEAK12d expression vector.

DETAILED DESCRIPTION OF THE INVENTION

The main object of the present invention is to provide novel, isolated polypeptides having chemotactic activity selected from the group consisting of:

a) the amino acid sequences SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16;

b) the mature form of the polypeptides SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16;

c) the polypeptides comprising the Cysteine-rich region of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, as indicated in fig. 9 and 10;

d) a variant of the amino acid sequence given by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 wherein any amino acid specified in the chosen sequence is non-

conservatively substituted, provided that no more than 15% of the amino acid residues in the sequence are so changed;

e) an active fragment, precursor, salt, or derivative of the amino acid sequences given in a) to d).

The novel polypeptides p1754 (SEQ ID NO: 2), p0711 (SEQ ID NO: 4), p2882 (SEQ ID NO: 6), p4711 (SEQ ID NO: 8), p4320 (SEQ ID NO: 10), p5008 (SEQ ID NO: 12), p0210 (SEQ ID NO: 14), and p4922 (SEQ ID NO: 16) were identified on the basis of a consensus sequence for human chemokines in which the number and the positioning of selected amino acids (initial methionine, cysteines, and hydrophobic residues) are defined for protein sequence having length comparable to known chemokines.

The totality of amino acid sequences obtained by translating the known ORFs in the human genome were challenged using this consensus sequence, and the positive hits were further screened for the presence of predicted specific structural and functional "signatures" (a N-terminal signal sequence and a C-terminal alpha helix), and finally selected by comparing sequence features with known chemokines. Therefore, the novel polypeptides of the invention can be predicted to have chemotactic activities.

The terms "active" and "activity" refer to the chemotactic-like properties predicted for the chemokine-like amino acid sequences SEQ ID NO: 2, 4, 6, 8, 10, 12 14, or 16 in the present patent application.

Protein sequences having the indicated number of non-conservative substitutions can be identified using commonly available bioinformatic tools (Mulder NJ and Apweiler R, 2002; Rehm BH, 2001).

In addition to such sequences, a series of polypeptides forms part of the disclosure of the invention. Being chemokines known to go through maturation processes including the proteolytic removal of N-terminal sequences (by signal peptidases and other proteolytic enzymes), the present patent application also claim the mature form of the polypeptides SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. As mature form is intended any polypeptide showing chemotactic activity and resulting from *in vivo* (by the expressing cells or animals) or *in vitro* (by modifying the purified polypeptides with specific enzymes) post-translational maturation processes. Mature forms of chemokines resulting from C-terminal processing are also known (Ehlert JE et al., 1998). Other alternative mature forms can also result from the addition of chemical groups such as sugars or phosphates.

A further group of polypeptides of the invention are the polypeptides comprising the Cysteine-rich region of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, as indicated in fig. 9 and 10, since the central Cysteine-rich region contains the essential structural and functional groups of chemokines.

Other claimed polypeptides are the active variants of the amino acid sequences given by SEQ ID NO: 2, 4, 6, 8, 10, 12 14, or 16 wherein any amino acid specified in the chosen sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues in the sequence are so changed. The indicated percentage has to be measured over the novel amino acid sequences disclosed in figures 1-8, and in particular over a segment of at least 40 amino acids containing the Cys-rich regions as indicated in figures 9 and 10.

In accordance with the present invention, any substitution should be preferably a "conservative" or "safe" substitution, which is commonly defined a substitution introducing an amino acids having sufficiently similar chemical properties (eg a basic,

positively charged amino acid should be replaced by another basic, positively charged amino acid), in order to preserve the structure and the biological function of the molecule.

The literature provide many models on which the selection of conservative amino acids substitutions can be performed on the basis of statistical and physico-chemical studies on the sequence and/or the structure of proteins (Rogov SI and Nekrasov AN, 2001). Protein design experiments have shown that the use of specific subsets of amino acids can produce foldable and active proteins, helping in the classification of amino acid "synonymous" substitutions which can be more easily accommodated in protein structure, and which can be used to detect functional and structural homologs and paralogs (Murphy LR et al., 2000). The groups of synonymous amino acids and the groups of more preferred synonymous amino acids are shown in Table I.

Active variants having comparable, or even improved, activity with respect of corresponding chemokines may result from conventional mutagenesis technique of the encoding DNA, from combinatorial technologies at the level of encoding DNA sequence (such as DNA shuffling, phage display/selection), or from computer-aided design studies, followed by the validation for the desired activities as described in the prior art.

Specific, non-conservative mutations can be also introduced in the polypeptides of the invention with different purposes. Mutations reducing the affinity of the chemokine-like polypeptide may increase its ability to be reused and recycled, potentially increasing its therapeutic potency (Robinson CR, 2002). Immunogenic epitopes eventually present in the polypeptides of the invention can be exploited for developing vaccines (Stevanovic S, 2002), or eliminated by modifying their sequence following known methods for selecting mutations for increasing protein stability, and

correcting them (van den Burg B and Eijsink V, 2002; WO 02/05146, WO 00/34317, WO 98/52976).

Further alternative polypeptides of the invention are active fragments, precursors, salt, or derivative of the amino acid sequences the above described sequences.

Fragments should present deletions of terminal or internal amino acids not altering their function, and should involve generally a few amino acids, e.g., under ten, and preferably under three, without removing or displacing amino acids which are critical to the functional conformation of the proteins.

The "precursors" are compounds which can be converted into the compounds of present invention by metabolic and enzymatic processing prior or after the administration to the cells or to the body.

The term "salts" herein refers to both salts of carboxyl groups and to acid addition salts of amino groups of the polypeptides of the present invention. Salts of a carboxyl group may be formed by means known in the art and include inorganic salts, for example, sodium, calcium, ammonium, ferric or zinc salts, and the like, and salts with organic bases as those formed, for example, with amines, such as triethanolamine, arginine or lysine, piperidine, procaine and the like. Acid addition salts include, for example, salts with mineral acids such as, for example, hydrochloric acid or sulfuric acid, and salts with organic acids such as, for example, acetic acid or oxalic acid. Any of such salts should have substantially similar activity to the peptides and polypeptides of the invention or their analogs.

The term "derivatives" as herein used refers to derivatives which can be prepared from the functional groups present on the lateral chains of the amino acid moieties or on the amino- or carboxy-terminal groups according to known methods. Such molecules can result also from other modifications which do not normally alter primary

sequence, for example *in vivo* or *in vitro* chemical derivativization of polypeptides (acetylation or carboxylation), those made by modifying the pattern of phosphorylation (introduction of phosphotyrosine, phosphoserine, or phosphothreonine residues) or glycosylation (by exposing the polypeptide to mammalian glycosylating enzymes) of a peptide during its synthesis and processing or in further processing steps. Alternatively, derivatives may include esters or aliphatic amides of the carboxyl-groups and N-acyl derivatives of free amino groups or O-acyl derivatives of free hydroxyl-groups and are formed with acyl-groups as for example alcanoyl- or aryl-groups.

The generation of the derivatives may involve a site-directed modification of an appropriate residue, in an internal or terminal position. The residues used for attachment should they have a side-chain amenable for polymer attachment (i.e., the side chain of an amino acid bearing a functional group, e.g., lysine, aspartic acid, glutamic acid, cysteine, histidine, etc.). Alternatively, a residue having a side chain amenable for polymer attachment can replace an amino acid of the polypeptide, or can be added in an internal or terminal position of the polypeptide. Also, the side chains of the genetically encoded amino acids can be chemically modified for polymer attachment, or unnatural amino acids with appropriate side chain functional groups can be employed. The preferred method of attachment employs a combination of peptide synthesis and chemical ligation. Advantageously, the attachment of a water-soluble polymer will be through a biodegradable linker, especially at the amino-terminal region of a protein. Such modification acts to provide the protein in a precursor (or "pro-drug") form, that, upon degradation of the linker releases the protein without polymer modification.

Polymer attachment may be not only to the side chain of the amino acid naturally occurring in a specific position of the antagonist or to the side chain of a natural or

unnatural amino acid that replaces the amino acid naturally occurring in a specific position of the antagonist, but also to a carbohydrate or other moiety that is attached to the side chain of the amino acid at the target position. Rare or unnatural amino acids can be also introduced by expressing the protein in specifically engineered bacterial strains (Bock A, 2001).

All the above indicated variants can be natural, being identified in organisms other than humans, or artificial, being prepared by chemical synthesis, by site-directed mutagenesis techniques, or any other known technique suitable thereof, which provide a finite set of substantially corresponding mutated or shortened peptides or polypeptides which can be routinely obtained and tested by one of ordinary skill in the art using the teachings presented in the prior art.

The novel amino acid sequences disclosed in the present patent application can be used to provide different kind of reagents and molecules. Examples of these compounds are binding proteins or antibodies that can be identified using their full sequence or specific fragments, such as antigenic determinants. Peptide libraries can be used in known methods (Tribbick G, 2002) for screening and characterizing antibodies or other proteins binding the claimed amino acid sequences, and for identifying alternative forms of the polypeptides of the invention having similar binding properties.

The present patent application discloses also fusion proteins comprising any of the polypeptides described above. These polypeptides should contain protein sequence heterologous to the one disclosed in the present patent application, without significatively impairing the chemotactic activity and possibly providing additional properties. Examples of such properties are an easier purification procedure, a longer lasting half-life in body fluids, an additional binding moiety, the maturation by means of

an endoproteolytic digestion, or extracellular localization. This latter feature is of particular importance for defining a specific group of fusion or chimeric proteins included in the above definition since it allows the claimed molecules to be localized in the space where not only isolation and purification of these polypeptides is facilitated, but also where generally chemokines and their receptor interact.

Design of the moieties, ligands, and linkers, as well methods and strategies for the construction, purification, detection and use of fusion proteins are disclosed in the literature (Nilsson J et al., 1997; Methods Enzymol, Vol. 326-328, Academic Press, 2000). The preferred one or more protein sequences which can be comprised in the fusion proteins belong to these protein sequences: membrane-bound protein, immunoglobulin constant region, multimerization domains, extracellular proteins, signal peptide-containing proteins, export signal-containing proteins. Features of these sequences and their specific uses are disclosed in a detailed manner, for example, for albumin fusion proteins (WO 01/77137), fusion proteins including multimerization domain (WO 01/02440, WO 00/24782), immunoconjugates (Garnett MC, 2001), or fusion protein providing additional sequences which can be used for purifying the recombinant products by affinity chromatography (Constans A, 2002; Burgess RR and Thompson NE, 2002; Lowe CR et al., 2001; J. Bioch. Biophy. Meth., vol. 49 (1-3), 2001; Sheibani N, 1999).

Studies on structure-activity relationships indicate that chemokines bind and activate receptors by making use of the amino-terminal region. Proteolytic digestion, mutagenesis, or chemical modifications directed to amino acids in this region can generate compounds having antagonistic activity (Loetscher P and Clark-Lewis I, 2001; Lambeir A et al., 2001, Proost P et al., 2001). Thus, antagonistic molecules resulting from specific modifications (deletions, non-conservative substitutions) of one or more

residues in the amino-terminal region or in other regions of the corresponding chemokine are considered having therapeutic potential for inflammatory and autoimmune diseases (WO 02/28419; WO 00/27880; WO 99/33989; Schwarz and Wells, 1999). Therefore, a further object of the present patent application is represented by such kind of antagonists generated by modifying the polypeptides of the invention.

The polypeptides of the invention can be used to generate and characterize ligands binding specifically to them. These molecules can be natural or artificial, very different from the chemical point of view (binding proteins, antibodies, molecularly imprinted polymers), and can be produced by applying the teachings in the art (WO 02/74938; Kuroiwa Y et al., 2002; Haupt K, 2002; van Dijk MA and van de Winkel JG, 2001; Gavilondo JV and Larrick JW, 2000). Such ligands can antagonize or inhibit the chemotactic activity of the polypeptide against which they have been generated. In particular, common and efficient ligands are represented by extracellular domain of a membrane-bound protein or antibodies, which can be in the form monoclonal, polyclonal, humanized antibody, or an antigen binding fragment.

The polypeptides and the polypeptide-based derived reagents described above can be in alternative forms, according to the desired method of use and/or production, such as active conjugates or complexes with a molecule chosen amongst radioactive labels, fluorescent labels, biotin, or cytotoxic agents.

Specific molecules, such as peptide mimetics, can be also designed on the sequence and/or the structure of a polypeptide of the invention. Peptide mimetics (also called peptidomimetics) are peptides chemically modified at the level of amino acid side chains, of amino acid chirality, and/or of the peptide backbone. These alterations

are intended to provide agonists or antagonists of the polypeptdes of the invention with improved preparation, potency and/or pharmacokinetics features.

For example, when the peptide is susceptible to cleavage by peptidases following injection into the subject is a problem, replacement of a particularly sensitive peptide bond with a non-cleavable peptide mimetic can provide a peptide more stable and thus more useful as a therapeutic. Similarly, the replacement of an L-amino acid residue is a standard way of rendering the peptide less sensitive to proteolysis, and finally more similar to organic compounds other than peptides. Also useful are amino-terminal blocking groups such as t-butyloxycarbonyl, acetyl, theyl, succinyl, methoxysuccinyl, suberyl, adipyl, azelayl, dansyl, benzyloxycarbonyl, fluorenylmethoxycarbonyl, methoxyazelayl, methoxyadipyl, methoxysuberyl, and 2,4-dinitrophenyl. Many other modifications providing increased potency, prolonged activity, easiness of purification, and/or increased half-life are disclosed in the prior art (WO 02/10195; Villain M et al., 2001).

Preferred alternative, synonymous groups for amino acids derivatives included in peptide mimetics are those defined in Table II. A non-exhaustive list of amino acid derivatives also include aminoisobutyric acid (Aib), hydroxyproline (Hyp), 1,2,3,4-tetrahydro-isoquinoline-3-COOH, indoline-2carboxylic acid, 4-difluoro-proline, L-thiazolidine-4-carboxylic acid, L-homoproline, 3,4-dehydro-proline, 3,4-dihydroxy-phenylalanine, cyclohexyl-glycine, and phenylglycine.

By "amino acid derivative" is intended an amino acid or amino acid-like chemical entity other than one of the 20 genetically encoded naturally occurring amino acids. In particular, the amino acid derivative may contain substituted or non-substituted, linear, branched, or cyclic alkyl moieties, and may include one or more heteroatoms. The

amino acid derivatives can be made de novo or obtained from commercial sources (Calbiochem-Novabiochem AG, Switzerland; Bachem, USA).

Various methodologies for incorporating unnatural amino acids derivatives into proteins, using both *in vitro* and *in vivo* translation systems, to probe and/or improve protein structure and function are disclosed in the literature (Dougherty DA, 2000). Techniques for the synthesis and the development of peptide mimetics, as well as non-peptide mimetics, are also well known in the art (Golebiowski A et al., 2001; Hruby VJ and Balse PM, 2000; Sawyer TK, in "Structure Based Drug Design", edited by Veerapandian P, Marcel Dekker Inc., pg. 557-663, 1997).

Another object of the present invention are isolated nucleic acids encoding for the polypeptides of the invention having chemotactic activity, the polypeptides binding to an antibody or a binding protein generated against them, the corresponding fusion proteins, or mutants having antagonistic activity as disclosed above. Preferably, these nucleic acids should comprise a DNA sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or the complement of said DNA sequences.

Alternatively, the nucleic acids of the invention should hybridize under high stringency conditions, or exhibits at least about 85% identity over a stretch of at least about 30 nucleotides, with a nucleic acid selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15 or a complement of said DNA sequences. 16. A purified nucleic acid according to claim 13 which to a nucleic acid selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or a complement of said nucleotide sequences. A further object of the present invention is therefore the polypeptides encoded by these purified nucleic acids.

The wording "high stringency conditions" refers to conditions in a hybridization reaction that facilitate the association of very similar molecules and consist in the

overnight incubation at 60§-65°C in a solution comprising 50 % formamide, 5X SSC (150 m M NaCl, 15 m M trisodium citrate), 50 mM sodium phosphate (p H 7 6), 5x Denhardt's solution, 10 % dextran sulphate, and 20 microgram/ml denatured, sheared salmon sperm DNA, followed by washing the filters in O.1X SSC at the same temperature.

These nucleic acids, including nucleotide sequences substantially the same, can be comprised in plasmids, vectors and any other DNA construct which can be used for maintaining, modifying, introducing, or expressing the encoding polypeptide. In particular, vectors wherein said nucleic acid molecule is operatively linked to expression control sequences can allow expression in prokaryotic or eukaryotic host cells of the encoded polypeptide.

The wording "nucleotide sequences substantially the same" includes all other nucleic acid sequences which, by virtue of the degeneracy of the genetic code, also code for the given amino acid sequences. In this sense, the literature provides indications on preferred or optimized codons for recombinant expression (Kane JF et al., 1995).

The nucleic acids and the vectors can be introduced into cells with different purposes, generating transgenic cells and organisms. A process for producing cells capable of expressing a polypeptide of the invention comprises genetically engineering cells with such vectors and nucleic acids.

In particular, host cells (e.g. bacterial cells) can be modified by transformation for allowing the transient or stable expression of the polypeptides encoded by the nucleic acids and the vectors of the invention. Alternatively, said molecules can be used to generate transgenic animal cells or non-human animals (by non- / homologous recombination or by any other method allowing their stable integration and

maintenance), having enhanced or reduced expression levels of the polypeptides of the invention, when the level is compared with the normal expression levels. Such precise modifications can be obtained by making use of the nucleic acids of the inventions and of technologies associated, for example, to gene therapy (Meth. Enzymol., vol. 346, 2002) or to site-specific recombinases (Kolb AF, 2002). Model systems based on the chemokine-like polypeptides disclosed in the present patent application for the systematic study of their function can be also generated by gene targeting into human cell lines (Bunz F, 2002).

The polypeptides of the invention can be prepared by any method known in the art, including recombinant DNA-related technologies, and chemical synthesis technologies. In particular, a method for making a polypeptide of the invention may comprise culturing a host or transgenic cell as described above under conditions in which the nucleic acid or vector is expressed, and recovering the polypeptide encoded by said nucleic acid or vector from the culture. For example, when the vector expresses the polypeptide as a fusion protein with an extracellular or signal-peptide containing proteins, the recombinant product can be secreted in the extracellular space, and can be more easily collected and purified from cultured cells in view of further processing or, alternatively, the cells can be directly used or administered.

The DNA sequence coding for the proteins of the invention can be inserted and ligated into a suitable episomal or non- / homologously integrating vectors, which can be introduced in the appropriate host cells by any suitable means (transformation, transfection, conjugation, protoplast fusion, electroporation, calcium phosphate-precipitation, direct microinjection, etc.). Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector, may be recognized and selected from those recipient cells which do not contain

the vector; the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

The vectors should allow the expression of the isolated or fusion protein including the polypeptide of the invention in the Prokaryotic or Eukaryotic host cells under the control of transcriptional initiation / termination regulatory sequences, which are chosen to be constitutively active or inducible in said cell. A cell line substantially enriched in such cells can be then isolated to provide a stable cell line.

For Eukaryotic hosts (e.g. yeasts, insect, plant, or mammalian cells), different transcriptional and translational regulatory sequences may be employed, depending on the nature of the host. They may be derived form viral sources, such as adenovirus, bovine papilloma virus, Simian virus or the like, where the regulatory signals are associated with a particular gene which has a high level of expression. Examples are the TK promoter of the Herpes virus, the SV40 early promoter, the yeast gal4 gene promoter, etc. Transcriptional initiation regulatory signals may be selected which allow for repression and activation, so that expression of the genes can be modulated. The cells stably transformed by the introduced DNA can be selected by introducing one or more markers allowing the selection of host cells which contain the expression vector. The marker may also provide for phototrophy to an auxotropic host, biocide resistance, e.g. antibiotics, or heavy metals such as copper, or the like. The selectable marker gene can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection.

Host cells may be either prokaryotic or eukaryotic. Preferred are eukaryotic hosts, e.g. mammalian cells, such as human, monkey, mouse, and Chinese Hamster Ovary (CHO) cells, because they provide post-translational modifications to proteins,

including correct folding and glycosylation. Also yeast cells can carry out post-translational peptide modifications including glycosylation. A number of recombinant DNA strategies exist which utilize strong promoter sequences and high copy number of plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences in cloned mammalian gene products and secretes peptides bearing leader sequences (i.e., pre-peptides).

The above mentioned embodiments of the invention can be achieved by combining the disclosure provided by the present patent application on the sequence of novel chemokine-like polypeptides with the knowledge of common molecular biology techniques.

Many books and reviews provides teachings on how to clone and produce recombinant proteins using vectors and Prokaryotic or Eukaryotic host cells, such as some titles in the series "A Practical Approach" published by Oxford University Press ("DNA Cloning 2: Expression Systems", 1995; "DNA Cloning 4: Mammalian Systems", 1996; "Protein Expression", 1999; "Protein Purification Techniques", 2001).

Moreover, updated and more focused literature provides an overview of the technologies for expressing polypeptides in a high-throughput manner (Chambers SP, 2002; Coleman TA, et al., 1997), of the cell systems and the processes used industrially for the large-scale production of recombinant proteins having therapeutic applications (Andersen DC and Krummen L, 2002, Chu L and Robinson DK, 2001), and of alternative eukaryotic expression systems for expressing the polypeptide of interest, which may have considerable potential for the economic production of the desired protein, such the ones based on transgenic plants (Giddings G, 2001) or the yeast *Pichia pastoris* (Lin Cereghino GP et al., 2002). Recombinant protein products can be rapidly monitored with various analytical technologies during purification to

verify the amount and the quantity of the expressed polypeptides (Baker KN et al., 2002), as well as to check if there is problem of bioequivalence and immunogenicity (Schellekens H, 2002; Gendel SM, 2002).

Totally synthetic chemokines are disclosed in the literature (Brown A et al., 1996), and many examples of chemical synthesis technologies, which can be effectively applied for the chemokine-like polypeptides of the invention given their short length, are available in the literature, as solid phase or liquid phase synthesis technologies. for example, the amino acid corresponding to the carboxy-terminus of the peptide to be synthetized is bound to a support which is insoluble in organic solvents, and by alternate repetition of reactions, one wherein amino acids with their amino groups and side chain functional groups protected with appropriate protective groups are condensed one by one in order from the carboxy-terminus to the amino-terminus, and one where the amino acids bound to the resin or the protective group of the amino groups of the peptides are released, the peptide chain is thus extended in this manner. Solid phase synthesis methods are largely classified by the tBoc method and the Fmoc method, depending on the type of protective group used. Typically used protective groups include tBoc (t-butoxycarbonyl), Cl-Z (2-chlorobenzyloxycarbonyl), Br-Z (2-bromobenzyloxycarbonyl), Bzl (benzyl), Fmoc (9-fluorenylmethoxycarbonyl), Mbh (4,4'-dimethoxydibenzhydryl), Mtr (4-methoxy-2,3,6-trimethylbenzenesulphonyl), Trt (trityl), Tos (tosyl), Z (benzyloxycarbonyl) and Cl2-Bzl (2,6-dichlorobenzyl) for the amino groups; NO2 (nitro) and Pmc (2,2,5,7,8-pentamethylchromane-6-sulphonyl) for the guanidino groups); and tBu (t-butyl) for the hydroxyl groups). After synthesis of the desired peptide, it is subjected to the de-protection reaction and cut out from the solid support. Such peptide cutting reaction may be carried with hydrogen fluoride or tri-fluoromethane sulfonic acid for the Boc method, and with TFA for the Fmoc method.

The purification of the polypeptides of the invention can be carried out by any one of the methods known for this purpose, i.e. any conventional procedure involving extraction, precipitation, chromatography, electrophoresis, or the like. A further purification procedure that may be used in preference for purifying the protein of the invention is affinity chromatography using monoclonal antibodies or affinity groups, which bind the target protein and which are produced and immobilized on a gel matrix contained within a column. Impure preparations containing the proteins are passed through the column. The protein will be bound to the column by heparin or by the specific antibody while the impurities will pass through. After washing, the protein is eluted from the gel by a change in pH or ionic strength. Alternatively, HPLC (High Performance Liquid Chromatography) can be used. The elution can be carried using a water-acetonitrile-based solvent commonly employed for protein purification.

The disclosure of the novel polypeptides of the invention, and the reagents disclosed in connection to them (antibodies, nucleic acids, cells) allows also to screen and characterize compounds that enhance or reduce their expression level into a cell or in an animal. Examples of compounds that can reduce or block the expression of the chemokine-like polypeptides are antisense oligonucleotides (Stein CA, 2001) or small interfering, double stranded RNA molecules that can trigger RNA interference-mediated silencing (Paddison PJ et al., 2002; Lewis DL et al., 2002). These compounds are intended as antagonists (in addition to the ones above described in connection to mutants and ligands) in the context of the possible mechanism of antagonism for blocking cytokine/chemokine-controlled pathways as defined in the literature (Choy EH and Panayi GS, 2001; Dower SK, 2000).

"Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized.

Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

The invention includes purified preparations of the compounds of the invention (polypeptides, nucleic acids, cells, etc.). Purified preparations, as used herein, refers to the preparations which conatin at least 1%, preferably at least 5%, by dry weight of the compounds of the invention.

The present patent application discloses a series of novel chemokine-like polypeptides and of related reagents having several possible applications. In particular, whenever an increase in the chemotactic activity of a polypeptide of the invention is desirable in the therapy or in the prevention of a disease, reagents such as the disclosed chemokine-like polypeptides, the corresponding fusion proteins and peptide mimetics, the encoding nucleic acids, the expressing cells, or the compounds enhancing their expression can be used.

Therefore, the present invention discloses pharmaceutical compositions for the treatment or prevention of diseases needing an increase in the chemotactic activity of a polypeptide of the invention, which contain one of the disclosed chemokine-like polypeptides, the corresponding fusion proteins and peptide mimetics, the encoding nucleic acids, the expressing cells, or the compounds enhancing their expression, as active ingredient. The process for the preparation of these pharmaceutical compositions comprises combining the disclosed chemokine-like polypeptides, the corresponding fusion proteins and peptide mimetics, the encoding nucleic acids, the expressing cells, or the compounds enhancing their expression, together with a pharmaceutically acceptable carrier. Methods for the treatment or prevention of

diseases needing an increase in the chemotactic activity of a polypeptide of the invention, comprise the administration of a therapeutically effective amount of the disclosed chemokine-like polypeptides, the corresponding fusion proteins and peptide mimetics, the encoding nucleic acids, the expressing cells, or the compounds enhancing their expression.

Amongst the reagents disclosed in the present patent application, the ligands, the antagonists or the compounds reducing the expression or the activity of polypeptides of the invention have several applications, and in particular they can be used in the therapy or in the diagnosis of a disease associated to the excessive chemotactic activity of a polypeptide of the invention.

Therefore, the present invention discloses pharmaceutical compositions for the treatment or prevention of diseases associated to the excessive chemotactic activity of a polypeptide of the invention, which contain one of the ligands, antagonists, or compounds reducing the expression or the activity of such polypeptides, as active ingredient. The process for the preparation of these pharmaceutical compositions comprises combining the ligand, the antagonist, or the compound, together with a pharmaceutically acceptable carrier. Methods for the treatment or prevention of diseases associated to the excessive chemotactic activity of the polypeptide of the invention, comprise the administration of a therapeutically effective amount of the antagonist, the ligand or of the compound.

The pharmaceutical compositions of the invention may contain, in addition to chemokine-like polypeptide or to the related reagent, suitable pharmaceutically acceptable carriers, biologically compatible vehicles and additives which are suitable for administration to an animal (for example, physiological saline) and eventually comprising auxiliaries (like excipients, stabilizers, adjuvants, or diluents) which facilitate

the processing of the active compound into preparations which can be used pharmaceutically.

The pharmaceutical compositions may be formulated in any acceptable way to meet the needs of the mode of administration. For example, of biomaterials, sugar-macromolecule conjugates, hydrogels, polyethylene glycol and other natural or synthetic polymers can be used for improving the active ingredients in terms of drug delivery efficacy. Technologies and models to validate a specific mode of administration are disclosed in literature (Davis BG and Robinson MA, 2002; Gupta P et al., 2002; Luo B and Prestwich GD, 2001; Cleland JL et al., 2001; Pillai O and Panchagnula R, 2001).

Polymers suitable for these purposes are biocompatible, namely, they are non-toxic to biological systems, and many such polymers are known. Such polymers may be hydrophobic or hydrophilic in nature, biodegradable, non-biodegradable, or a combination thereof. These polymers include natural polymers (such as collagen, gelatin, cellulose, hyaluronic acid), as well as synthetic polymers (such as polyesters, polyorthoesters, polyanhydrides). Examples of hydrophobic non-degradable polymers include polydimethyl siloxanes, polyurethanes, polytetrafluoroethylenes, polyethylenes, polyvinyl chlorides, and polymethyl methaerylates. Examples of hydrophilic non-degradable polymers include poly(2-hydroxyethyl methacrylate), polyvinyl alcohol, poly(N-vinyl pyrrolidone), polyalkylenes, polyacrylamide, and copolymers thereof. Preferred polymers comprise as a sequential repeat unit ethylene oxide, such as polyethylene glycol (PEG).

Any accepted mode of administration can be used and determined by those skilled in the art to establish the desired blood levels of the active ingredients. For example, administration may be by various parenteral routes such as subcutaneous,

intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, oral, or buccal routes. The pharmaceutical compositions of the present invention can also be administered in sustained or controlled release dosage forms, including depot injections, osmotic pumps, and the like, for the prolonged administration of the polypeptide at a predetermined rate, preferably in unit dosage forms suitable for single administration of precise dosages.

Parenteral administration can be by bolus injection or by gradual perfusion over time. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions, which may contain auxiliary agents or excipients known in the art, and can be prepared according to routine methods. In addition, suspension of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions that may contain substances increasing the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. Optionally, the suspension may also contain stabilizers. Pharmaceutical compositions include suitable solutions for administration by injection, and contain from about 0.01 to 99.99 percent, preferably from about 20 to 75 percent of active compound together with the excipient.

The wording "therapeutically effective amount" refers to an amount of the active ingredients that is sufficient to affect the course and the severity of the disease, leading to the reduction or remission of such pathology. The effective amount will depend on the route of administration and the condition of the patient.

The wording "pharmaceutically acceptable" is meant to encompass any carrier, which does not interfere with the effectiveness of the biological activity of the active ingredient and that is not toxic to the host to which is administered. For example, for parenteral administration, the above active ingredients may be formulated in unit dosage form for injection in vehicles such as saline, dextrose solution, serum albumin and Ringer's solution. Carriers can be selected also from starch, cellulose, talc, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, magnesium stearate, sodium stearate, glycerol monostearate, sodium chloride, dried skim milk, glycerol, propylene glycol, water, ethanol, and the various oils, including those of petroleum, animal, vegetable or synthetic origin (peanut oil, soybean oil, mineral oil, sesame oil).

It is understood that the dosage administered will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. The dosage will be tailored to the individual subject, as is understood and determinable by one of skill in the art. The total dose required for each treatment may be administered by multiple doses or in a single dose. The pharmaceutical composition of the present invention may be administered alone or in conjunction with other therapeutics directed to the condition, or directed to other symptoms of the condition. Usually a daily dosage of active ingredient is comprised between 0.01 to 100 milligrams per kilogram of body weight per day. Ordinarily 1 to 40 milligrams per kilogram per day given in divided doses or in sustained release form is effective to obtain the desired results. Second or subsequent administrations can be performed at a dosage, which is the same, less than, or greater than the initial or previous dose administered to the individual.

Apart from the methods having a therapeutic or a production purpose, several other methods can make use of the chemokine-like polypeptides and of the related reagents disclosed in the present patent application.

In a first example, a method for screening candidate compounds effective to treat a disease related to a chemokine-like polypeptides of the invention, comprises:

(a)contacting host cells expressing such polypeptide, transgenic non-human animals, or transgenic animal cells having enhanced or reduced expression levels of the polypeptide, with a candidate compound and

(b)determining the effect of the compound on the animal or on the cell.

In a second example, a method for identifying a candidate compound as an antagonist/inhibitor or agonist/activator of a polypeptide of the invention comprises:

(a) contacting the polypeptide, the compound, and a mammalian cell or a mammallian cell membrane; and

(b) measuring whether the molecule blocks or enhances the interaction of the polypeptide, or the response that results from such interaction, with the mammalian cell or the mammalian cell membrane.

In a third example, methods for determining the activity and/or the presence of the polypeptide of the invention in a sample, can detect either the polypeptide or the encoding RNA/DNA. Thus, such a method comprises:

(a) providing a protein-containing sample;

(b) contacting said sample with a ligand of the invention; and

(c) determining the presence of said ligand bound to said polypeptide, thereby determining the activity and/or the presence of polypeptide in said sample.

Alternatively, the method comprises:

(a) providing a nucleic acids-containing sample;

(b) contacting said sample with a nucleic acid of the invention; and

(c) determining the hybridization of said nucleic acid with a nucleic acid into the sample, thereby determining the presence of the nucleic acid in the sample.

In this sense, primer sequences containing the sequences SEQ ID NO: 17-28 (Table III) can be used as well for determining the presence or the amount of a transcript or of a nucleic acid encoding a polypeptide of invention in a sample by means of Polymerase Chain Reaction amplification.

A further object of the present invention are kits for measuring the activity and/or the presence of chemokine-like polypeptide of the invention in a sample comprising one or more of the reagents disclosed in the present patent application: a chemokine-like polypeptide of the invention, an antagonist, ligand or peptide mimetic, an isolated nucleic acid or the vector, a pharmaceutical composition, an expressing cell, a compound increasing or decreasing the expression levels, and/or primer sequences containing the sequences SEQ ID NO: 17-28.

Those kits can be used for *in vitro* diagnostic or screenings methods, and their actual composition should be adapted to the specific format of the sample (e.g. biological sample tissue from a patient), and the molecular species to be measured. For example, if it is desired to measure the concentration of the chemokine-like polypeptide, the kit may contain an antibody and the corresponding protein in a purified form to compare the signal obtained in Western blot. Alternatively, if it is desired to measure the concentration of the transcript for the chemokine-like polypeptide, the kit may contain a specific nucleic acid probe designed on the corresponding ORF sequence, or may be in the form of nucleic acid array containing such probe, or the primer sequences disclosed as SEQ ID NO: 17-28 (Table III). The kits can be also in the form of protein-, peptide mimetic-, or cell-based microarrays (Templin MF et al.,

2002; Pellois JP et al., 2002; Blagoev B and Pandey A, 2001), allowing high-throughput proteomics studies, by making use of the proteins, peptide mimetics and cells disclosed in the present patent application.

The present patent application discloses novel chemokine-like polypeptides and a series of related reagents that may be useful, as active ingredients in pharmaceutical compositions appropriately formulated, in the treatment or prevention of diseases such as cell proliferative disorders, autoimmune/inflammatory disorders, cardiovascular disorders, neurological disorders, developmental disorders, metabolic disorder, infections and other pathological conditions. In particular, given the known properties of chemokines, the disclosed polypeptides and reagents should address conditions involving abnormal or defective cell migration. Non-limitative examples of such conditions are the following: arthritis, rheumatoid arthritis (RA), psoriatic arthritis, osteoarthritis, systemic lupus erythematosus (SLE), systemic sclerosis, scleroderma, polymyositis, glomerulonephritis, fibrosis, lung fibrosis and inflammation, allergic or hypersensitvity diseases, dermatitis, asthma, chronic obstructive pulmonary disease (COPD), inflammatory bowel disease (IBD), Crohn's diseases, ulcerative colitis, multiple sclerosis, septic shock, HIV infection, transplant rejection, wound healing, metastasis, endometriosis, hepatitis, liver fibrosis, cancer, analgesia, and vascular inflammation related to atherosclerosis.

The therapeutic applications of the polypeptides of the invention and of the related reagents can be evaluated (in terms or safety, pharmacokinetics and efficacy) by the means of the *in vivo / in vitro* assays making use of animal cell, tissues and models (Coleman RA et al., 2001; Li AP, 2001; Methods Mol. Biol vol. 138, "Chemokines Protocols", edited by Proudfoot AI et al., Humana Press Inc., 2000; Methods Enzymol, vol. 287 and 288, Academic Press, 1997), or by the means of *in*

silico / computational approaches (Johnson DE and Wolfgang GH, 2000), known for the validation of chemokines and other biological products during drug discovery and preclinical development.

All publications, patents and patent applications cited herein are incorporated in full by reference for all purposes.

The invention will now be described with reference to the specific embodiments by means of the following Examples, which should not be construed as in any way limiting the present invention. The content of the description comprises all modifications and substitutions which can be practiced by a person skilled in the art in light of the above teachings and, therefore, without extending beyond the meaning and purpose of the claims.

EXAMPLES

Example 1: Selection of chemokine-like open reading frames (ORFs) from human genome

Perl (Practical Extraction and Report Language) is a programming language having powerful pattern matching functions into large text data files allowing the extraction of information from genomic DNA sequences, starting from a alpha-numerical expression describing a defined consensus sequence (Stein LD, 2001).

A Perl script was used to retrieve novel open reading frames (ORFs), having chemokine-like features, in a FASTA-formatted sequence file containing the NCBI genome (build 28). After translating the genomic DNA sequence into the six possible reading frames (3 forward and 3 reverse), each of these translated sequences was then tested for a match against a pattern designed to detect to chemokine-like proteins,

which was elaborated comparing multiple sequence alignments of known chemokines. The following pattern, fitting all the aligned sequences, was adopted:

$\{M\}-\{X\}_{3-12}-\{L \text{ or } I \text{ or } V\}_{1-3}-\{X\}_{0-2}-\{L \text{ or } I \text{ or } V\}_{2-4}-\{X\}_{0-2}-\{L \text{ or } I \text{ or } V\}_{1-3}-\{X\}_{10-30}-\{C\}-(X)_{0-3}-C-(X)_{20-40}-C-\{X\}_{12-20}-\{C\}-\{X\}_{15-40}$ STOP

The letter(s) between brackets represented alternative amino acids (in one-letter code) which should be present the number of times indicated in subscript characters. This expression, which describes the entire family of sequences on the basis of the respective positioning of the initial methionine, hydrophobic residues, and conserved cysteines on the linear sequence, can be transformed in Perl language as follows:

M[^*]{3,12}[LIV]{1,3}[^*]{0,2}[LIV]{2,4}[^*]{0,2}[LIV]{1,3}[^*]{10,30}C[^*]{0,3}C[^*]{20,40}C[^*]{12,20}C[^*]{15,40}[*]

A total of FASTA-formatted 7974 ORFs matching the pattern were compared to known proteins present in protein databases (SwissProt/Trembl and Derwent GENESEQ) using a rapid searching program for local alignments between a query and a hit sequence based on Basic Local Alignment Search Tool (BLAST, BLASTX) and ClustalW algorithms (Altschul SF et al., 1990; Pearson WR and Miller W, 1992; Gish W and States DJ, 1993). BLAST parameters used were: Comparison matrix = BLOSUM62; word length = 3; .E value cutoff = 10; Gap opening and extension = default; No filter.

The sequences obtained from this first screening were further selected using additional criteria. 2441 ORFs showing at least 70% of homology with known proteins in protein databases were eliminated. The remaining 5533 ORFs were filtered using 2 neural network-based algorithms developed for the prediction (probability at least 0.7)

of a N-terminal signal peptide and of an alpha helix secondary structure having at least 5 amino acids within the C-terminal 30 amino acids (a hallmark of the IL8-like fold) with high confidence. The resulting 253 ORFs, which were predicted as containing these features, were transformed in text format and were compared to known chemokines, searching manually for the best alignments. This further refinement, based on the qualitative assessment of the alignments, led to the selection of eight chemokine-like encoding ORFs presenting sequence length, cysteine spacing, and predicted N-terminal signal sequence and C-terminal alpha helix comparable to known chemokines.

The DNA sequence GNSQ_1754 (SEQ ID NO: 1), belonging to human chromosome 13, contains an ORF encoding for the 98-amino acid long protein sequence p1754 (SEQ ID NO: 2), which, according to the prediction, presents a 22-amino acid long signal sequence and an alpha helix covering the residues 70-79 (figure 1).

The DNA sequence GNSQ_0711 (SEQ ID NO: 3), belonging to human chromosome 16, contains an ORF encoding for the 109-amino acid long protein sequence p0711 (SEQ ID NO: 4), which, according to the prediction, presents a 17-amino acid long signal sequence and an alpha helix covering the residues 98-106 (figure 2).

The DNA sequence GNSQ_2882 (SEQ ID NO: 5), belonging to human chromosome 6, contains an ORF encoding for the 107-amino acid long protein sequence p2882 (SEQ ID NO: 6), which, according to the prediction, presents a 18-amino acid long signal sequence and an alpha helix covering the residues 96-104 (figure 3).

The DNA sequence GNSQ_4711 (SEQ ID NO: 7), belonging to human chromosome 3, contains an ORF encoding for the 102-amino acid long protein

sequence p4711 (SEQ ID NO: 8), which, according to the prediction, presents a 22-amino acid long signal sequence and an alpha helix covering the residues 83-97 (figure 4).

The DNA sequence GNSQ_4320 (SEQ ID NO: 9), belonging to human chromosome 3, contains an ORF encoding for the 101-amino acid long protein sequence p4320 (SEQ ID NO: 10), which, according to the prediction, presents a 16-amino acid long signal sequence and an alpha helix covering the residues 90-98 (figure 5).

The DNA sequence GNSQ_5008 (SEQ ID NO: 11), belonging to human chromosome 12, contains an ORF encoding for the 112-amino acid long protein sequence p5008 (SEQ ID NO: 12), which, according to the prediction, presents a 17-amino acid long signal sequence and an alpha helix covering the residues 95-109 (figure 6).

The DNA sequence GNSQ_0210 (SEQ ID NO: 13), belonging to human chromosome 7, contains an ORF encoding for the 127-amino acid long protein sequence p0210 (SEQ ID NO: 14), which, according to the prediction, presents a 16-amino acid long signal sequence and an alpha helix covering the residues 94-113 (figure 7).

The DNA sequence GNSQ_4922 (SEQ ID NO: 15), belonging to human chromosome 10, contains an ORF encoding for the 91-amino acid long protein sequence p4922 (SEQ ID NO: 14), which, according to the prediction, presents a 23-amino acid long signal sequence and an alpha helix covering the residues 67-74 (figure 8).

Amongst these sequences characterized as encoding chemokine-like polypeptides, five of them (p1754, p0711, p2882, p0210, and p4922) present a central

Cys-rich region in which the first two Cysteines are separated by 1-3 amino acids (figure 9). The remaining three sequences (p4711, p4320, and p5008) present two adjacent Cysteines at the beginning of such region (figure 10).

Example 2: Cloning of the novel chemokine-like ORFs from human genomic DNA

Six of the eight above-defined chemokine-like ORFs (GNSQ_1754, GNSQ_4922, GNSQ_5008, GNSQ_0210, GNSQ_0711, and GNSQ_4320) were first cloned from human genomic DNA into a cloning vector, and then transferred into an expression vector using Polymerase Chain Reaction (PCR), with pairs of forward/reverse primers specific for each ORF (see arrows in figure 1, 2, and 5-8).

The cloning primers (CL series; Table III), having a length comprised between 19 and 25 bases, were designed for amplifying each ORF, using human genomic DNA as template. The forward primers start from the initial ATG or a few nucleotides before. The reverse primers are complementary to the 3' end of the ORF, including the stop codon.

The PCR was performed by mixing the following components in each ORF-specific reaction (total volume of 50 µl in double-distilled water):

150 ng human genomic DNA (Clontech)

1.2 µM primers (0.6 µM each primer)

240 µM dNTP (Invitrogen)

0.5 µl AmpliTaq (2.5 Units; Applied Biosystems)

5 AmpliTaq buffer 10X (Applied Biosystems)

The PCR reactions were performed using an initial denaturing step if 94°C for 2 minutes, followed by 30 cycles:

94°C for 30 seconds

55°C for 30 seconds

72°C for 30 seconds

After a final elongation step of 72°C for 10 minutes, the PCR products were directly subcloned into the pCRII-TOPO vector using the TOPO™ cloning system (Invitrogen), according to manufacturer's standard protocol. The TOPO cloning system is a variation of the TA cloning system allowing the rapid cloning of PCR products, taking advantage from the fact that Taq polymerase leaves a single Adenosine at the 3' end of PCR products. Since the TOPO vector has single-stranded Thymine overhangs, Topoisomerase I enzyme is able to join the T-ends of the vector to the A-overhangs of the PCR product, which can be used without any purification step.

The resulting plasmids (pCRTOPO-ORF series) were used to transform *E. coli* cells (TOP10F', Invitrogen, supplied with the TOPO TA Cloning Kit), obtaining several clones for each ORF. Plasmid DNA was isolated using a commercial kit (WIZARD Plasmid Minipreps: Promega) and sequenced to verify the identity of the amplified and cloned sequence with the originally selected human genomic DNA sequence.

The plasmids containing the desired sequences were used in a further round of PCR reactions necessary for transferring the ORFs into the expression vector pEAK12d (figure 11), which allows the expression of the cloned insert under the control of EF-1α promoter and in frame with a 6-His Tag sequence, using the Gateway cloning system (Invitrogen).

The expression vector pEAK12D was constructed by modifying pEAK12 (Edge Biosystems). This vector was digested with HindIII and NotI, made blunt ended with Klenow and dephosphorylated using calf-intestinal alkaline phosphatase. After dephosphorylation, the vector was ligated to blunt ended Gateway reading frame cassette C (Gateway vector conversion system, Invitrogen cat no. 11828-019) which

contains AttR recombination sites flanking the ccdB gene (marker for negative selction of non-recombinant plasmids) and chloramphenicol resistance. The resulting plasmids were used to transform DB3.1 *E. coli* cells, which allow propagation of vectors containing the ccdB gene. Miniprep DNA was isolated from several of the resultant colonies and digested with AseI / EcoRI to identify clones yielding a 670 bp fragment, obtainable only when the cassette had been inserted in the correct orientation. The resultant plasmid was called pEAK12D.

Two series of primers (Table IV) were designed to add the ATTB1 and ATTB2 recombination sites (necessary for the integration in the expression vector) at the 5' and 3' end, respectively, of the ORF-containing insert. In the first series of primers (EX1 series), the original ORF-specific CL primers were modified by adding, at the 5' end, the sequence AAGCAGGCTTCGCCACC (for forward primers) or GTGATGGTGATGGTG (for reverse primers, but after eliminating the nucleotides complementary to the stop codon). In the second series of primers (EX2 series), the original ORF-specific CL primers were modified by adding, at the 5' end, the sequence GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGCCACC (for forward primers) or GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAATGGTGATGGTGATGGTG (for reverse primers, but after eliminating the nucleotides complementary to the stop codon). These reverse primers contain the codons for the 6-His tag which result fused in frame with the ORFs at their C- terminal end.

The PCR amplification was performed in 2 consecutive reactions. The first one was performed by mixing the following components (total volume 50 µl in double-distilled water):

25 ng pCRTOPO-ORF vector

5mM dNTP (Invitrogen)

0.5 µl Pfx DNA polymerase (Invitrogen)

0.5 µl each EX1 primer (100µM)

5µl 10X Pfx polymerase buffer(Invitrogen)

The PCR reactions were performed using an initial denaturing step of 95°C for 2 minutes, followed by 10 cycles:

94°C for 15 seconds

68°C for 30 seconds

The PCR products were purified using the Wizard PCR prep DNA purification system (Promega), and added as templates in a second PCR reaction including the following components (total volume 50 µl in double-distilled water):

10 µl purified PCR product

5mM dNTP (Invitrogen)

0.5 µl Pfx DNA polymerase (Invitrogen)

0.5 µl each EX2 primer (100µM)

5µl 10X Pfx polymerase buffer (Invitrogen)

The PCR reactions were performed an initial denaturing step of 95°C for 1 minute, followed by 4 cycles:

94°C for 15 seconds

50°C for 30 seconds

68°C for 3 minutes 30 seconds

Then the following conditions were applied for 25 cycles:

94°C for 15 seconds

55°C for 30 seconds

68°C for 3 minutes 30 seconds.

The DNA fragments resulting from the PCR reactions were purified as described before and recombined into the pEAK12d vector using the Gateway system.

First, the following 10 µl reactions were assembled:

pDONR-201 (0.1 µg/µl)	1.5 µl
PCR product	5 µl
BP buffer	2 µl
BP enzyme mix	1.5 µl

After being incubated at room temperature for 1 hour, the reaction was stopped by adding proteinase K (1 µl, 2 µg) and incubating at 37°C for further 10 minutes.

An aliquot of this reaction (2 µl) was used for transforming *E. coli* cells (strain DH10B) by electroporation. Plasmid DNA was prepared for 4 clones for each ORF and used for parallel 10 µl recombination reactions containing:

pEAK12d (0.1 µg / µl)	1.5 µl
Plasmid DNA	1.5 µl
ddH20	3.5 µl
LR buffer	2 µl
LR enzyme mix	1.5 µl

After being incubated at room temperature for 1 hour, the reaction was stopped by adding proteinase K (1 µl, 2 µg) and incubating at 37°C for further 10 minutes. An aliquot of this reaction (1 µl) was used for transforming DH10B *E. coli* cells by electroporation. The clones containing the correct insert were identified first by performing colony PCR on 3 colonies using the forward and reverse vector primers pEAK12d F1 (GCCAGCTTGGCACTTGATGT) and pEAK12d R1 (GATGGAGGTGGACGTGTCAG), then confirmed by sequencing the insert with the same primer.

Example 3: Expression and purification of the His-tagged chemokine-like polypeptides in mammalian cells

Human Embryonic Kidney cells expressing the Epstein-Barr virus Nuclear Antigen (HEK293-EBNA) were seeded in T225 flasks (50 ml at a density of $2x10^5$ cells/ml) from 16 to 20 hours prior to transfection, which was performed using the cationic polymer reagent JetPEI™ (PolyPlus-transfection; 2 µl/µg of plasmid DNA). For each flask, 113 µg of the ORF-specific pEAK12d plasmid, which were prepared using CsCl (Sambrook, J et al. "Molecular Cloning, a laboratory manual"; 2nd edition. 1989; Cold Spring Harbor Laboratory Press), were co-transfected with 2.3 µg of a plasmid acting as positive control since it expresses Green Fluorescent Protein (GFP). The plasmids, diluted in 230 µl of JetPEI™ solution, were added to 4.6 ml of NaCl 150 mM, vortexed and incubated for 30 minutes at room temperature. This transfection mix was then added to the T225 flask and incubated at 37°C for 6 days. An aliquot of the cultures was then exposed to UV irradiation to check the transfection efficiency by evaluating GFP fluorescence.

Culture medium from HEK293-EBNA cells transfected with the same plasmids were pooled and 100 ml of the medium were diluted to 200 ml with 100 ml of ice-cold buffer A (50 mM NaH_2PO_4; 600 mM NaCl; 8.7 % (w/v) glycerol, pH 7.5), which is the same buffer used for equilibrating the affinity column on which His-tagged proteins were subsequently immobilized and eluted. The solution was filtered through a 0.22 µm sterile filter (Millipore) and kept at 4°C in 250 ml sterile square media bottles until further processing.

Two consecutive chromatography procedures were applied to the samples at 4°C using an HPLC-based system (Perfusion Chromatography™, PerSeptive

Biosystems) including a VISION workstation (BioCAD™ series), POROS™ chromatographic media, and an external 250 ml-sample loader (Labomatic).

In the first chromatography step, a Ni-metal affinity column (0.83 ml, POROS 20 MC) was first regenerated with 30 column volumes of EDTA solution (100 mM EDTA; 1 M NaCl; pH 8.0), and then recharged with Ni ions through washing with 15 column volumes of the Ni solution (100 mM $NiSO_4$). The column is subsequently washed with 10 column volumes of buffer A, 7 column volumes of buffer B (50 mM NaH_2PO_4; 600 mM NaCl; 8.7 % (w/v) glycerol, 400 mM; imidazole, pH 7.5), and finally equilibrated with 15 column volumes of buffer A containing 15 mM imidazole. The sample loader charged the protein-containing solution onto the Ni metal affinity column at a flow rate of 10 ml/min. The column was then washed with 12 column volumes of Buffer A, followed by 28 column volumes of Buffer A containing a concentration of imidazole (20 mM) allowing the elution of contaminating proteins that are loosely attached to the Ni-column. The His-tagged protein is finally eluted with 10 column volumes of Buffer B at a flow rate of 2 ml/min, collecting collected 1.6 ml fractions.

In the second chromatography step, a gel-filtration column (10 ml G-25 Sephadex) was regenerated with 2 ml of buffer D (137 mM NaCl; 2.7 mM KCl; 1.5 mM KH_2PO_4; 8 mM Na_2HPO_4; 1 M NaCl; pH 7.2), and then equilibrated with 2 column volumes of buffer C (137 mM NaCl; 2.7 mM KCl; 1.5 mM KH_2PO_4; 8 mM Na_2HPO_4; 20 % (w/v) glycerol; pH 7.4) before injecting the Ni-column peak fractions onto this column. The sample is eluted with buffer C and the desalted sample is recovered in 2.2 ml fractions. The peak fractions from the gel-filtration column were filtered through a 0.22 µm sterile centrifugation filter (Millipore) and aliquots (20 µl) were analyzed in parallel on SDS-PAGE (4-12 % NuPAGE gel; Novex) by Coomassie staining and by Western blot with antibodies recognizing His-tags. Protein concentrations were

determined in the samples that show detectable protein bands by Coomassie staining, using the BCA Protein Assay kit (Pierce) and Bovine Serum Albumin as standard.

The gel for the Western blot analysis was electrotransferred to a nitrocellulose membrane at 290 mA at 4°C for 1 hour. The membrane is blocked with 5 % milk powder in PBS (137 mM NaCl; 2.7 mM KCl; 1.5 mM KH_2PO_4; 8 mM Na_2HPO_4;pH 7.4), and subsequently incubated with a mixture of 2 rabbit polyclonal anti-His antibodies (G-18 and H-15, 0.2 µg/ml each; Santa Cruz) at 4°C overnight. After a further 1 hour incubation at room temperature, the membrane was washed with PBS containing 0.1% Tween-20 (3 x 10 min), and then exposed to a secondary HRP-conjugated anti-rabbit antibody (DAKO) at room temperature for 2 hours. After washing in PBS containing 0.1% Tween-20 (3 x 10 minutes), the ECL kit (Amersham Pharmacia) was used to detect the antibodies immobilized onto the membrane, comparing the film with the image of the Coomassie stained gel.

Example 4: Cell- and Animal-based assay for the validation and characterization of the chemokine-like polypeptides.

Several assays have been developed for testing specificity, potency, and efficacy of chemokines using cell cultures or animal models, for example *in vitro* chemotaxis assays (Proudfoot AE et al., 2001; Lusti-Narasimhan M et al., 1995), or mouse ear swelling (Garrigue JL et al., 1994). Many other assays and technologies for generating useful tools and products (antibodies, transgenic animals, radiolabeled proteins, etc.) have been described in reviews and books dedicated to chemokines (Methods Mol. Biol vol. 138, "Chemokines Protocols", edited by Proudfoot AI et al., Humana Press Inc., 2000; Methods Enzymol, vol. 287 and 288, Academic Press, 1997), and can be used to verify, in a more precise manner, the biological activities of

the chemokine-like polypeptides of the invention and related reagents in connection with possible therapeutic or diagnostic methods and uses.

TABLE I

Amino Acid	Synonymous Groups	More Preferred Synonymous Groups
Ser	Gly, Ala, Ser, Thr, Pro	Thr, Ser
Arg	Asn, Lys, Gln, Arg, His	Arg, Lys, His
Leu	Phe, Ile, Val, Leu, Met	Ile, Val, Leu, Met
Pro	Gly, Ala, Ser, Thr, Pro	Pro
Thr	Gly, Ala, Ser, Thr, Pro	Thr, Ser
Ala	Gly, Thr, Pro, Ala, Ser	Gly, Ala
Val	Met, Phe, Ile, Leu, Val	Met, Ile, Val, Leu
Gly	Ala, Thr, Pro, Ser, Gly	Gly, Ala
Ile	Phe, Ile, Val, Leu, Met	Ile, Val, Leu, Met
Phe	Trp, Phe,Tyr	Tyr, Phe
Tyr	Trp, Phe,Tyr	Phe, Tyr
Cys	Ser, Thr, Cys	Cys
His	Asn, Lys, Gln, Arg, His	Arg, Lys, His
Gln	Glu, Asn, Asp, Gln	Asn, Gln
Asn	Glu, Asn, Asp, Gln	Asn, Gln
Lys	Asn, Lys, Gln, Arg, His	Arg, Lys, His
Asp	Glu, Asn, Asp, Gln	Asp, Glu
Glu	Glu, Asn, Asp, Gln	Asp, Glu
Met	Phe, Ile, Val, Leu, Met	Ile, Val, Leu, Met
Trp	Trp, Phe,Tyr	Trp

TABLE II

Amino Acid	Synonymous Groups
Ser	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Arg	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-.Met, D-Ile, Orn, D-Orn
Leu	D-Leu, Val, D-Val, AdaA, AdaG, Leu, D-Leu, Met, D-Met
Pro	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid
Thr	D-Thr, Ser, D-Ser, allo-Thr, Met,D-Met, Met(O), D-Met(O), Val, D-Val
Ala	D-Ala, Gly, Aib, B-Ala, Acp, L-Cys, D-Cys
Val	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met, AdaA, AdaG
Gly	Ala, D-Ala, Pro, D-Pro, Aib, .beta.-Ala, Acp
Ile	D-Ile, Val, D-Val, AdaA, AdaG, Leu, D-Leu, Met, D-Met
Phe	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, AdaA, AdaG, cis-3,4, or 5-phenylproline, Bpa, D-Bpa
Tyr	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Cys	D-Cys, S--Me--Cys, Met, D-Met, Thr, D-Thr
Gln	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Asn	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Lys	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Asp	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Glu	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Met	D-Met, S--Me--Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val

TABLE III

SEQ ID NO:	NAME	DIRECTION	5'->3' SEQUENCE
17	CL_1754_5	Forward	ATGAATGTCATTGTTTTACA
18	CL_1754_3	Reverse	CTACCAACCTGTACAGCATG
19	CL_4922_5	Forward	CTGACTATGATGAGGGTGCTAAGGC
20	CL_4922_3	Reverse	TCAAATTGCTGGGAAAGTTCTCAGG
21	CL_5008_5	Forward	CATGATCTTTGGCCTGCTAATC
22	CL_5008_3	Reverse	TTAAAGGGAAAGTAATAGGAG
23	CL_0210_5	Forward	CTATGGGCTTTGTTGTTCTATG
24	CL_0210_3	Reverse	TCAGAAAAATTCTAACAAAATTG
25	CL_0711_5	Forward	ATGGTTATTCCACATCTTG
26	CL_0711_3	Reverse	TCATCTCTGTTGCAGCAAACG
27	CL_4320_5	Forward	ATGTTATTTACTTTATTATTC
28	CL_4320_3	Reverse	TCACAGAAAAATCAAAGAGG

TABLE IV

SEQ ID NO:	NAME	DIRECTION	5'-3' SEQUENCE
29	EX1_1754_5	Forward	AAGCAGGCTTCGCCACCATGAATGTCATTGTTTTACA
30	EX1_1754_3	Reverse	GTGATGGTGATGGTGCCAACCTGTACAGCATG
31	EX1_4922_5	Forward	AAGCAGGCTTCGCCACCCTGACTATGATGAGGGTGCTAAGGC
32	EX1_4922_3	Reverse	GTGATGGTGATGGTGAATTGCTGGGAAAGTTCTCAGG
33	EX1_5008_5	Forward	AAGCAGGCTTCGCCACCCATGATCTTTGGCCTGCTAATC
34	EX1_5008_3	Reverse	GTGATGGTGATGGTGAAGGGAAAGTAATAGGAG
35	EX1_0210_5	Forward	AAGCAGGCTTCGCCACCCTATGGGCTTTGTTGTTCTATG
36	EX1_0210_3	Reverse	GTGATGGTGATGGTGGAAAAATTCTAACAAAATTG
37	EX1_0711_5	Forward	AAGCAGGCTTCGCCACCATGGTTATTCCACATCTTG
38	EX1_0711_3	Reverse	GTGATGGTGATGGTGTCTCTGTTGCAGCAAACG
39	EX1_4320_5	Forward	AAGCAGGCTTCGCCACCATGTTATTTACTTTATTATTC
40	EX1_4320_3	Reverse	GTGATGGTGATGGTGCAGAAAAATCAAAGAGG
41	EX2_1754_5	Forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGCCACCATGAATGTC ATTGTTTTACA
42	EX2_1754_3	Reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAATGGTGATGGTGA TGGTGCCAACCTGTACAGCATG
43	EX2_4922_5	Forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGCCACCCTGACTATG ATGAGGGTGCTAAGGC
44	EX2_4922_3	Reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAATGGTGATGGTGA TGGTGAATTGCTGGGAAAGTTCTCAGG
45	EX2_5008_5	Forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGCCACCCATGATCTT TGGCCTGCTAATC
46	EX2_5008_3	Reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAATGGTGATGGTGA TGGTGAAGGGAAAGTAATAGGAG
47	EX2_0210_5	Forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGCCACCCTATGGGCT TTGTTGTTCTATG
48	EX2_0210_3	Reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAATGGTGATGGTGA TGGTGGAAAAATTCTAACAAAATTG
49	EX2_0711_5	Forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGCCACCATGGTTATT CCACATCTTG
50	EX2_0711_3	Reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAATGGTGATGGTGA TGGTGTCTCTGTTGCAGCAAACG
51	EX2_4320_5	Forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGCCACCATGTTATTT ACTTTATTATTC
52	EX2_4320_3	Reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCAATGGTGATGGTGA TGGTGCAGAAAAATCAAAGAGG

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CLAIMS

1. An isolated polypeptide having chemotactic activity selected from the group consisting of:

   a) the amino acid sequences SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16;

   b) the mature form of the polypeptides SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16;

   c) the polypeptides comprising the Cysteine-rich region of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, as indicated in fig. 9 and 10;

   d) the active variants of the amino acid sequence given by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 wherein any amino acid specified in the chosen sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues in the sequence are so changed;

   e) the active fragment, precursor, salt, or derivative of the amino acid sequences given in a) to d).

2. The polypeptide of claim 1 that is a naturally occurring allelic variant of the sequence given by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

3. The polypeptide of claim 2, wherein the variant is the translation of a single nucleotide polymorphism.

4. The polypeptide of any of the claims from 1 to 3, wherein the polypeptide binds specifically an antibody or a binding protein generated against SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 or a fragment thereof.

5 A fusion protein comprising a polypeptide according to any of the claims from 1 to 4.

6 The fusion proteins of claim 6 wherein said proteins further comprise one or more amino acid sequence belonging to these protein sequences: membrane-bound protein, immunoglobulin constant region, multimerization domains, extracellular proteins, signal peptide-containing proteins, export signal-containing proteins.

7 An antagonist of a polypeptide of any of the claims from 1 to 4, wherein said antagonist comprises an amino acid sequence resulting from the non-conservative substitution and/or the deletion of one or more residues into the corresponding polypeptide.

8 A ligand which binds specifically to a polypeptide according to any one of claims 1 to 4.

9 The ligand of claim 8 that antagonizes or inhibits the chemotactic activity of a polypeptide according to any one of claims 1 to 4.

10 A ligand according to claim 11 which is a monoclonal antibody, a polyclonal antibody, a humanized antibody, an antigen binding fragment, or the extracellular domain of a membrane-bound protein.

11 The polypeptides of any of the claims from 1 to 7 or of claim 10, wherein said polypeptides are in the form of active conjugates or complexes with a molecule chosen amongst radioactive labels, fluorescent labels, biotin, or cytotoxic agents.

12 A peptide mimetic designed on the sequence and/or the structure of a polypeptide according to any one of claims 1 to 4.

13 An isolated nucleic acid encoding for an isolated polypeptide selected from the group consisting of:

a) the polypeptides having chemotactic activity of any of the claims from 1 to 4;

b) the fusion proteins of claim 5 or 6; or

c) the antagonists of claim 7.

14. The nucleic acid of Claim 13, comprising a DNA sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or the complement of said DNA sequences.

15. A purified nucleic acid which:

a) hybridizes under high stringency conditions; or

b) exhibits at least about 85% identity over a stretch of at least about 30 nucleotides

with a nucleic acid selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or a complement of said DNA sequences

16. A vector comprising a nucleic acid of any of Claims from 13 to 15.

17. The vector of claim 16, wherein said nucleic acid molecule is operatively linked to expression control sequences allowing expression in prokaryotic or eukaryotic host cells of the encoded polypeptide.

18. The polypeptides encoded by the purified nucleic acids of claim 15.

19. A process for producing cells capable of expressing a polypeptide of any the claims from 1 to 7 or of claim 18, comprising genetically engineering cells with a vector or a nucleic acid according to any of the claims from 13 to 17.

20. A host cell transformed with a vector or a nucleic acid according to any of the claims from 13 to 17.

21. A transgenic animal cell that has been transformed with a vector or a nucleic acid according to any of the claims from 13 to 17, having enhanced or reduced expression levels of a polypeptide according to any one of claims from 1 to 4.

22. A transgenic non-human animal that has been transformed to have enhanced or reduced expression levels of a polypeptide according to any one of claims from 1 to 4.

23. A method for making a polypeptide of any the claims from 1 to 7 comprising culturing a cell of claim 20 or 21 under conditions in which the nucleic acid or

vector is expressed, and recovering the polypeptide encoded by said nucleic acid or vector from the culture.

24. A compound that enhances the expression level of a polypeptide according to any one of claims from 1 to 4 into a cell or in an animal.

25. A compound that reduces the expression level of a polypeptide according to any one of claims from 1 to 4 into a cell or in an animal.

26. The compound of claim 24 that is an antisense oligonucleotide or a small interfering RNA.

27. Purified preparations containing a polypeptide of any of the claims from 1 to 6 or claim 18, an antagonist of claim 7, a ligand of any of the claims from 8 to 10, peptide mimetic of claim 12, a nucleic acid of any of the claims from 13 to 17, a cell of claim 20 or 21, or a compound of any of the claims from 24 to 26.

28. Use of a polypeptide of any of the claims from 1 to 6 or claim 18, a peptide mimetic of claim 12, a nucleic acid of any of the claims from 13 to 17, a cell of claim 20 or 21, or a compound of claim 24, in the therapy or in the prevention of a disease when the increase in the chemotactic activity of a polypeptide of any of the claims from 1 to 4 is needed.

29. Pharmaceutical compositions for the treatment or prevention of diseases needing an increase in the chemotactic activity of a polypeptide of any of the claims from

1 to 6 or claim 18, a peptide mimetic of claim 12, a nucleic acid of any of the claims from 13 to 17, a cell of claim 20 or 21, or a compound of claim 24, as active ingredient.

30. Process for the preparation of pharmaceutical compositions, which comprises combining a polypeptide of any of the claims from 1 to 6 or claim 18, a peptide mimetic of claim 12, a nucleic acid of any of the claims from 13 to 17, a cell of claim 20 or 21, or a compound of claim 24, together with a pharmaceutically acceptable carrier.

31. Method for the treatment or prevention of diseases needing an increase in the chemotactic activity of a polypeptide of any of the claims from 1 to 4, comprising the administration of a therapeutically effective amount of a polypeptide of any of the claims from 1 to 6 or claim 18, a peptide mimetic of claim 12, a nucleic acid of any of the claims from 13 to 17, a cell of claim 20 or 21, or a compound of claim 24.

32. Use of an antagonist of claim 7, a ligand of any of the claims from 8 to 10, or of a compound of claims 25 or 26, in the therapy or in the prevention of a disease associated to the excessive chemotactic activity of a polypeptide of any of the claims from 1 to 4.

33. Pharmaceutical compositions for the treatment or prevention of a disease associated to the excessive chemotactic activity of a polypeptide of any of the

claims from 1 to 4, containing an antagonist of claim 7, a ligand of any of the claims from 8 to 10, or of a compound of claims 25 or 26, as active ingredient.

34. Process for the preparation of pharmaceutical compositions for the treatment or prevention of diseases associated to the excessive chemotactic activity of a polypeptide of any of the claims from 1 to 4, which comprises combining an antagonist of claim 7, a ligand of any of the claims from 8 to 10, or of a compound of claims 25 or 26, together with a pharmaceutically acceptable carrier.

35. A method for the treatment or prevention of diseases related to the polypeptide of any of the claims from 1 to 4, comprising the administration of a therapeutically effective amount of an antagonist of claim 7, a ligand of any of the claims from 8 to 10, or of a compound of claims 25 or 26.

36. A method for screening candidate compounds effective to treat a disease related to the chemokine-like polypeptides of any of the claims from 1 to 4, comprising:

(a) contacting a cell of claim 20, a transgenic animal cell of claim 21, or a transgenic non-human animal according to claim 22, having enhanced or reduced expression levels of the polypeptide, with a candidate compound and

(b) determining the effect of the compound on the animal or on the cell.

37. A method for identifying a candidate compound as an antagonist/inhibitor or agonist/activator of a polypeptide of any of the claims 1 to 4 comprising:

(a) contacting said polypeptide, said compound, and a mammalian cell or a mammallian cell membrane capable of binding the polypeptide; and

(b) measuring whether the molecule blocks or enhances the interaction of the polypeptide, or the response that results from such interaction, with the mammalian cell or the mammalian cell membrane.

38. A method for determining the activity and/or the presence of the polypeptide of any the claims from 1 to 4 in a sample, the method comprising:

(a) providing a protein-containing sample;

(b) contacting said sample with a ligand of any of the claims from 8 to 10; and

(c) determining the presence or said ligand bound to said polypeptide.

39. A method for determining the presence or the amount of a transcript or of a nucleic acid encoding the polypeptide of any the claims from 1 to 4 in a sample, the method comprising:

(a) providing a nucleic acids-containing sample;

(b) contacting said sample with a nucleic acid of any of the claims 13 to 17; and

(c) determining the hybridization of said nucleic acid with a nucleic acid into the sample.

40. Use of the primer sequences containing the sequences SEQ ID NO: 17-28 for determining the presence or the amount of a transcript or of a nucleic acid encoding a polypeptide of any the claims from 1 to 4 in a sample by Polymerase Chain Reaction

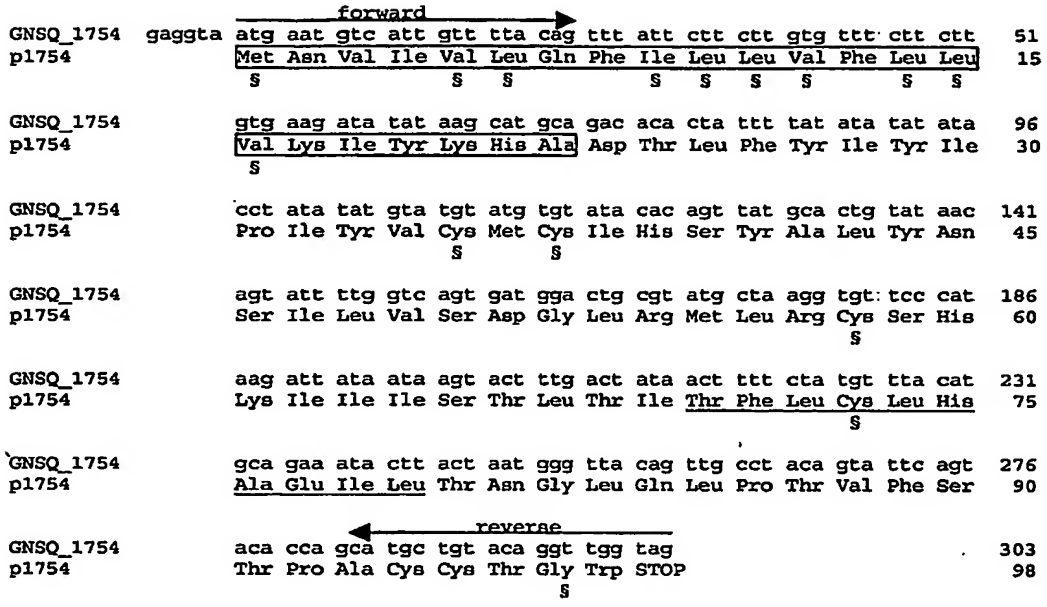
41. A kit for measuring the activity and/or the presence of the chemokine-like polypeptides of any of the claims from 1 to 4 in a sample comprising one or more

of the following reagents: a polypeptide of any of the claims from 1 to 6 or clam 18, an antagonist of claim 7, a ligand of any of the claims from 8 to 10, a polypeptide of claim 11, a peptide mimetic of claim 12, a nucleic acid of any of the claims from 13 to 17, a cell of claim 20 or 21, a compound of any of the claims from 24 to 26, a pharmaceutical composition of claims 29 or 33, or primer sequences containing the sequences SEQ ID NO: 17-28.

ABSTRACT

The present invention discloses open reading frames (ORFs) in human genome encoding for novel chemokines-like polypeptides, and reagents related thereto including variants, mutants and fragments of said polypeptides, as well as ligands and antagonists directed against them. The invention provides methods for identifying and making these molecules, for preparing pharmaceutical compositions containing them, and for using them in the diagnosis, prevention and treatment of diseases

Figure 1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p1754 Pro Ile Tyr Val Cys Met Cys Ile His Ser Tyr Ala Leu Tyr Asn 45
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p1754 Ser Ile Leu Val Ser Asp Gly Leu Arg Met Leu Arg Cys Ser His 60
GNSQ_1754 aag att ata ata agt act ttg act ata act ttt cta tgt tta cat 231
p1754 Lys Ile Ile Ile Ser Thr Leu Thr Ile Thr Phe Leu Cys Leu His 75
GNSQ_1754 gca gaa ata ctt act aat ggg tta cag ttg cct aca gta ttc agt 276
p1754 Ala Glu Ile Leu Thr Asn Gly Leu Gln Leu Pro Thr Val Phe Ser 90
reverse
GNSQ_1754 aca cca gca tgc tgt aca ggt tgg tag 303
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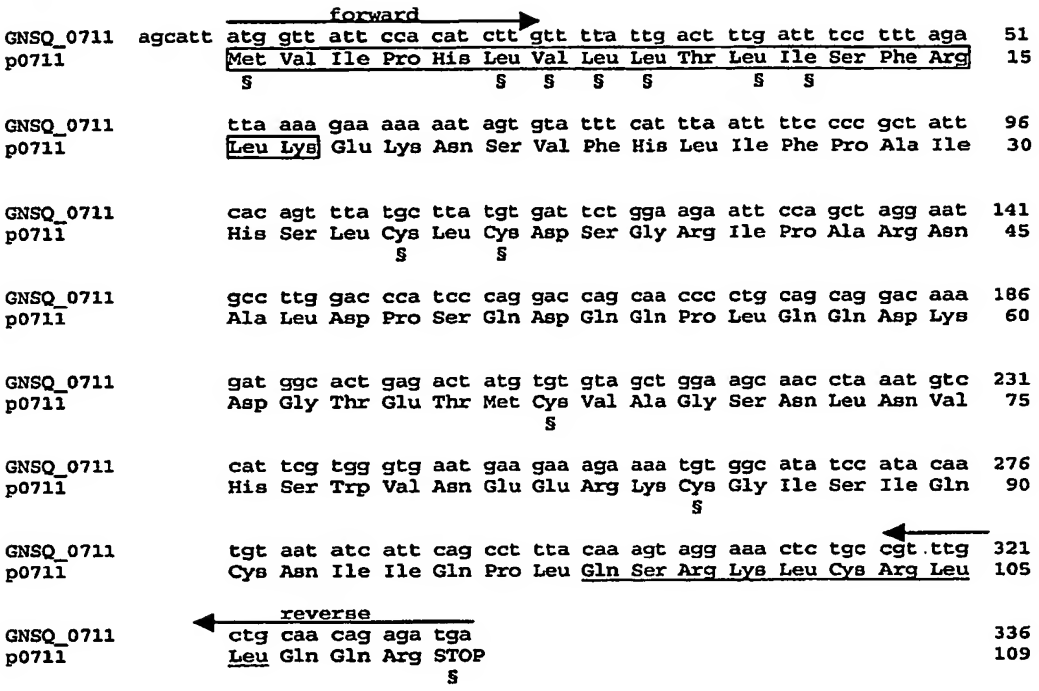
Figure 2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p0711 His Ser Trp Val Asn Glu Glu Arg Lys Cys Gly Ile Ser Ile Gln 90
GNSQ_0711 tgt aat atc att cag cct tta caa agt agg aaa ctc tgc cgt ttg 321
p0711 Cys Asn Ile Ile Gln Pro Leu Gln Ser Arg Lys Leu Cys Arg Leu 105
reverse
GNSQ_0711 ctg caa cag aga tga 336
p0711 Leu Gln Gln Arg STOP 109

Figure 3

```
GNSQ_2882  ggaagt atg agt cct agt tta ttc ttc att ttt aag att gtt ttg gct att   51
p2882              Met Ser Pro Ser Leu Phe Phe Ile Phe Lys Ile Val Leu Ala Ile   15
                    §                           §         §   §   §       §

GNSQ_2882          gtg gat tcc ctg caa ttc tat atg aat ttc gaa tca gtt tgt cga   96
p2882              Val Asp Ser Leu Gln Phe Tyr Met Asn Phe Glu Ser Val Cys Arg   30
                    §                                                   §

GNSQ_2882          tgt ctg caa aaa atc tct gtg att ctg ata ggg att gct ttt aac  141
p2882              Cys Leu Gln Lys Ile Ser Val Ile Leu Ile Gly Ile Ala Phe Asn   45
                    §

GNSQ_2882          ctg tgt aac gat ttg ggg agt att gtc att tta aca gtg tta tgt  186
p2882              Leu Cys Asn Asp Leu Gly Ser Ile Val Ile Leu Thr Val Leu Cys   60
                                                                         §

GNSQ_2882          att cta atc cat gaa tat gaa ata tat ttc ctt ttg ttt aga tct  231
p2882              Ile Leu Ile His Glu Tyr Glu Ile Tyr Phe Leu Leu Phe Arg Ser   75

GNSQ_2882          ttg att ttt tca tta tgt ttt ata gtt cca gag tat agt aag ttt  276
p2882              Leu Ile Phe Ser Leu Cys Phe Ile Val Pro Glu Tyr Ser Lys Phe   90
                                        §

GNSQ_2882          tgc aat ttt tat gtt aaa ttt att ctt aag aat tta ttt ttg atg  321
p2882              Cys Asn Phe Tyr Val Lys Phe Ile Leu Lys Asn Leu Phe Leu Met  105

GNSQ_2882          cta tca taa                                                 330
p2882              Leu Ser STOP                                                107
                          §
```

Figure 4

```
GNSQ_4711  tctagg atg gta act cct atc tgg aca ctt ttc att tgt tac tgt ttg acc   51
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                   §                                                       §

GNSQ_4711         tct ttg ctt gta tta cag gct ata ttt aaa gaa ata gat aac att   96
p4711             Ser Leu Leu Val Leu Gln Ala Ile Phe Lys Glu Ile Asp Asn Ile   30
                       §   §   §   §

GNSQ_4711         ctc tct gag gtt gat tta aac caa cat cct gta cgt tgc tgc tat  141
p4711             Leu Ser Glu Val Asp Leu Asn Gln His Pro Val Arg Cys Cys Tyr   45
                                                                  §   §

GNSQ_4711         agc ttc cca aca ttt tgt gta gag ggg atg cta ttg aag ttg tgt  186
p4711             Ser Phe Pro Thr Phe Cys Val Glu Gly Met Leu Leu Lys Leu Cys   60

GNSQ_4711         ttt aat atg gag cca cac tgt ttt ctt tct ctg acc cag tct aca  231
p4711             Phe Asn Met Glu Pro His Cys Phe Leu Ser Leu Thr Gln Ser Thr   75
                                          §

GNSQ_4711         gtc agc ctg tcc caa ggc tgc cat cta ttc tct gtg ttt gtg cag  276
p4711             Val Ser Leu Ser Gln Gly Cys His Leu Phe Ser Val Phe Val Gln   90
                                          §

GNSQ_4711         ctc atc tgg aca gct cat ctg gac aga cac aaa gaa tag          315
p4711             Leu Ile Trp Thr Ala His Leu Asp Arg His Lys Glu STOP         102
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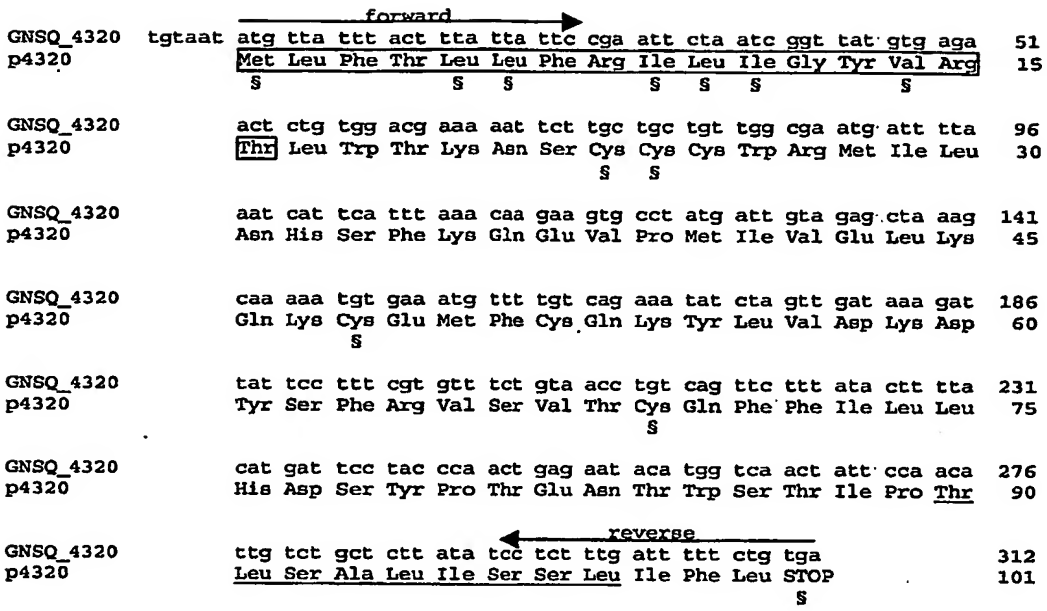
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GNSQ_4320 caa aaa tgt gaa atg ttt tgt cag aaa tat cta gtt gat aaa gat 186
p4320 Gln Lys Cys Glu Met Phe Cys Gln Lys Tyr Leu Val Asp Lys Asp 60
GNSQ_4320 tat tcc ttt cgt gtt tct gta acc tgt cag ttc ttt ata ctt tta 231
p4320 Tyr Ser Phe Arg Val Ser Val Thr Cys Gln Phe Phe Ile Leu Leu 75
GNSQ_4320 cat gat tcc tac cca act gag aat aca tgg tca act att cca aca 276
p4320 His Asp Ser Tyr Pro Thr Glu Asn Thr Trp Ser Thr Ile Pro Thr 90
reverse
GNSQ_4320 ttg tct gct ctt ata tcc tct ttg att ttt ctg tga 312
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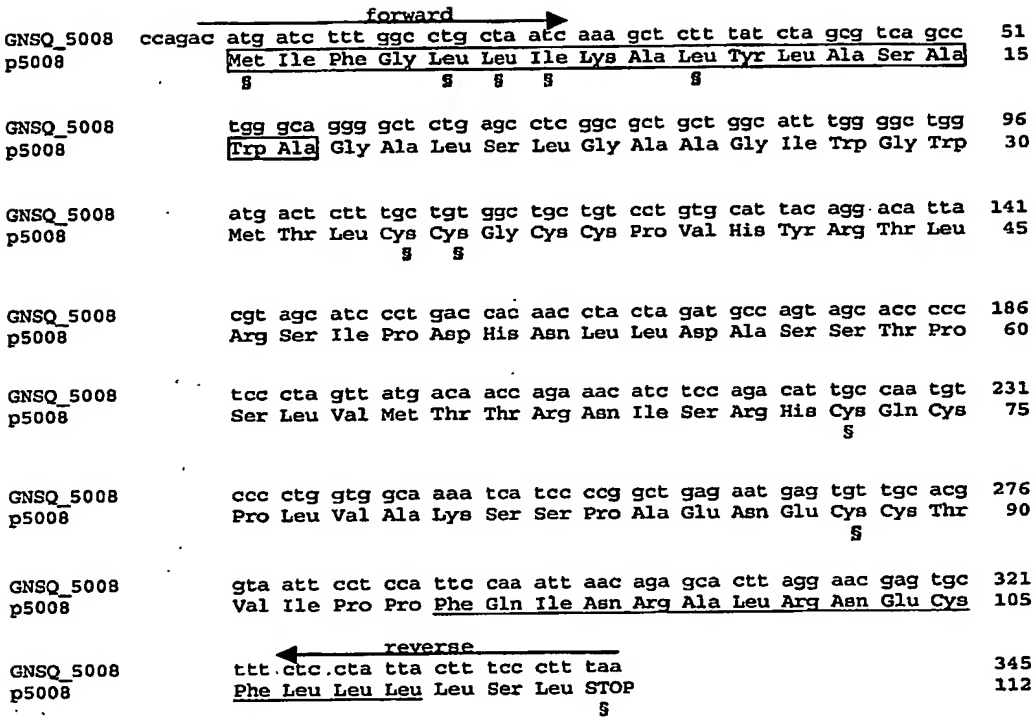
Figure 6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p5008 Trp Ala Gly Ala Leu Ser Leu Gly Ala Ala Gly Ile Trp Gly Trp 30
GNSQ_5008 atg act ctt tgc tgt ggc tgc tgt cct gtg cat tac agg aca tta 141
p5008 Met Thr Leu Cys Cys Gly Cys Cys Pro Val His Tyr Arg Thr Leu 45
GNSQ_5008 cgt agc atc cct gac cac aac cta cta gat gcc agt agc acc ccc 186
p5008 Arg Ser Ile Pro Asp His Asn Leu Leu Asp Ala Ser Ser Thr Pro 60
GNSQ_5008 tcc cta gtt atg aca acc aga aac atc tcc aga cat tgc caa tgt 231
p5008 Ser Leu Val Met Thr Thr Arg Asn Ile Ser Arg His Cys Gln Cys 75
GNSQ_5008 ccc ctg gtg gca aaa tca tcc ccg gct gag aat gag tgt tgc acg 276
p5008 Pro Leu Val Ala Lys Ser Ser Pro Ala Glu Asn Glu Cys Cys Thr 90
GNSQ_5008 gta att cct cca ttc caa att aac aga gca ctt agg aac gag tgc 321
p5008 Val Ile Pro Pro Phe Gln Ile Asn Arg Ala Leu Arg Asn Glu Cys 105
reverse
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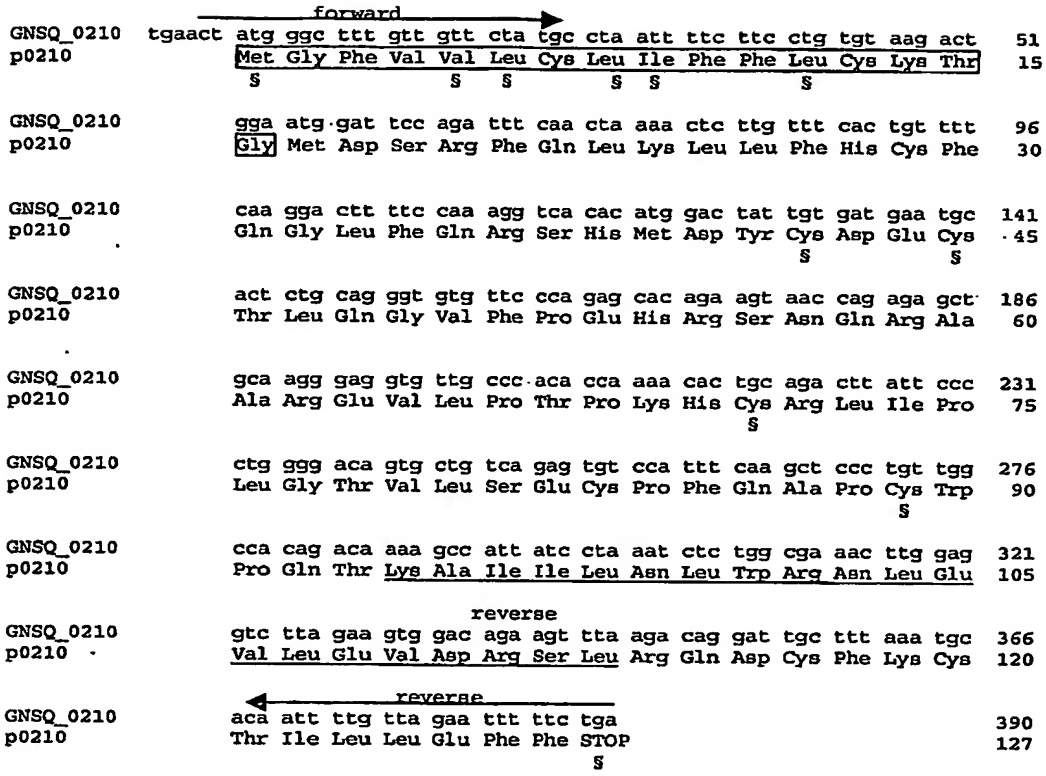
Figure 7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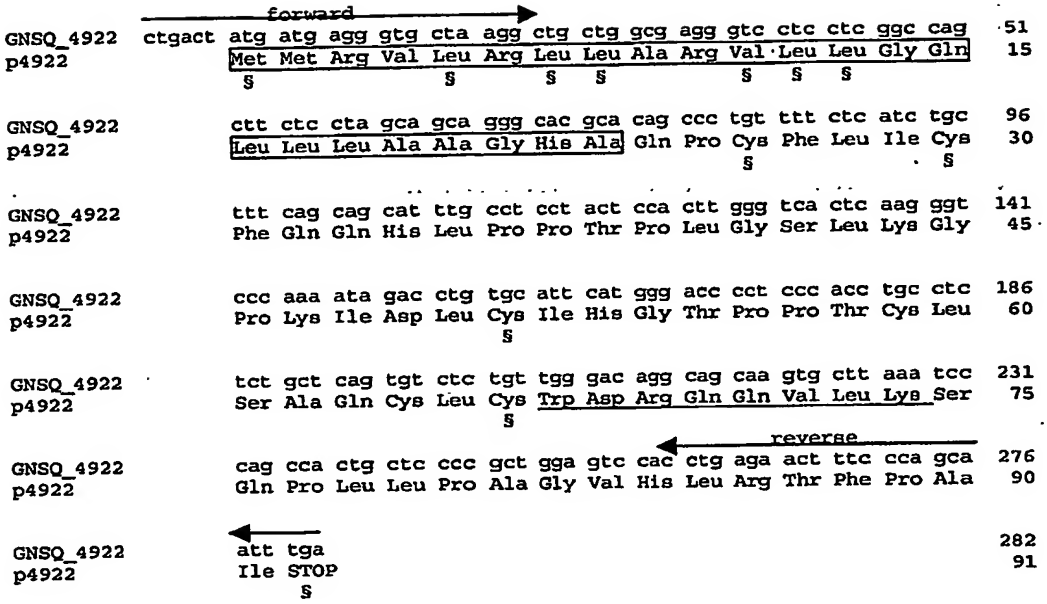
p0210 Gly Met Asp Ser Arg Phe Gln Leu Lys Leu Leu Phe His Cys Phe 30
GNSQ_0210 caa gga ctt ttc caa agg tca cac atg gac tat tgt gat gaa tgc 141
p0210 Gln Gly Leu Phe Gln Arg Ser His Met Asp Tyr Cys Asp Glu Cys 45
GNSQ_0210 act ctg cag ggt gtg ttc cca gag cac aga agt aac cag aga gct 186
p0210 Thr Leu Gln Gly Val Phe Pro Glu His Arg Ser Asn Gln Arg Ala 60
GNSQ_0210 gca agg gag gtg ttg ccc aca cca aaa cac tgc aga ctt att ccc 231
p0210 Ala Arg Glu Val Leu Pro Thr Pro Lys His Cys Arg Leu Ile Pro 75
GNSQ_0210 ctg ggg aca gtg ctg tca gag tgt cca ttt caa gct ccc tgt tgg 276
p0210 Leu Gly Thr Val Leu Ser Glu Cys Pro Phe Gln Ala Pro Cys Trp 90
GNSQ_0210 cca cag aca aaa gcc att atc cta aat ctc tgg cga aac ttg gag 321
p0210 Pro Gln Thr Lys Ala Ile Ile Leu Asn Leu Trp Arg Asn Leu Glu 105
reverse
GNSQ_0210 gtc tta gaa gtg gac aga agt tta aga cag gat tgc ttt aaa tgc 366
p0210 Val Leu Glu Val Asp Arg Ser Leu Arg Gln Asp Cys Phe Lys Cys 120
reverse
GNSQ_0210 aca att ttg tta gaa ttt ttc tga 390
p0210 Thr Ile Leu Leu Glu Phe Phe STOP 127

Figure 8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GNSQ_4922 ctt ctc cta gca gca ggg cac gca cag ccc tgt ttt ctc atc tgc 96
p4922 Leu Leu Leu Ala Ala Gly His Ala Gln Pro Cys Phe Leu Ile Cys 30
GNSQ_4922 ttt cag cag cat ttg cct cct act cca ctt ggg tca ctc aag ggt 141
p4922 Phe Gln Gln His Leu Pro Pro Thr Pro Leu Gly Ser Leu Lys Gly 45
GNSQ_4922 ccc aaa ata gac ctg tgc att cat ggg acc cct ccc acc tgc ctc 186
p4922 Pro Lys Ile Asp Leu Cys Ile His Gly Thr Pro Pro Thr Cys Leu 60
GNSQ_4922 tct gct cag tgt ctc tgt tgg gac agg cag caa gtg ctt aaa tcc 231
p4922 Ser Ala Gln Cys Leu Cys Trp Asp Arg Gln Gln Val Leu Lys Ser 75
reverse
GNSQ_4922 cag cca ctg ctc ccc gct gga gtc cac ctg aga act ttc cca gca 276
p4922 Gln Pro Leu Leu Pro Ala Gly Val His Leu Arg Thr Phe Pro Ala 90
GNSQ_4922 att tga 282
p4922 Ile STOP 91

Figure 9

N-Terminal Region

```
CXCL1          MARAALS--AAPSNPR---LLRVALLLLLLVAAGRRAAG
CXCL2          MARATLS--AAPSNPR---LLRVALLLLLLVAASRRAAG
CXCL3          MAHATLS--AAPSNPR---LLRVALLLLLLVGSRRAAGAS
CXCL4          MS--SAF--CASRPG----LLFLGLLLLPLVVAFASA
CXCL5          MSLLSSR--AARVPGPSSSLCALLVLLLLLTQPGPIASA
CXCL6          MSLPSSR--AARVPGPSGSLCALLALLLLLTPPGPLASA
CXCL7          MSLRLDTTPSCNSARPLHALQVLLLLSLLLTALASSTKGQTKRNLAKGKEE
CXCL8          MT---SKL-A---------V-ALLAAFLI-SAALCEG
CXCL9          MKKSG-------------VLFLLGIILLVLIGVQG
CXCL10         MNQTA-------------I-LICCLIFLTLSGIQG
CXCL11         MSVKGM------------AIALAVILCATVVQG
p1754          MNVI--------------VLQFILLVFLLVKIYKHADTLFYI
p0711          MVIPH-------------LV-LLTLISFRLKEKNSVFH
p2882          MSPS--------------L-FFIFKIVLAIVDSL
p0210          MGFVVLCLIFFLCKTGMDSRFQLKLLFHCFQGL
p4922          MMR---------------VLRLLARVLLGQLLLAA
```

Cys-rich region

```
CXCL1      ASVATELRCQ--CLQTLQGIHPKN-IQSVNVKSPG------PHCAQTE--VIATLKNGRKA---C
CXCL2      APLATELRCQ--CLQTLQGIHLKN-IQSVKVKSPG------PHCAQTE--VIATLKNGQKA---C
CXCL3        VVTELRCQ--CLQTLQGIHLKN-IQSVNVRSPG------PHCAQTE--VIATLKNGKKA---C
CXCL4     EAEEDGDLQCL--CVKTTSQVRPRH-ITSLEVIKAG------PHCPTAQ--LIATLKNGRK---IC
CXCL5   GPAAAVLRELRCV--CLQTTQGVHPKM-ISNLQVFAIG------PQCSKVE--VVASLKNGKE---IC
CXCL6   GPVSAVLTELRCT--CLRVTLRVNPKT-IGKLQVFPAG------PQCSKVE--VVASLKNGKQ---VC
CXCL7   SLDSDLYAELRCM--CIKTTSGIHPKN-IQSLEVIGKG------THCNQVE--VIATLKDGRK---IC
CXCL8   AVLPRSAKELRCQ--CIKTYSKPFHPKFIKELRVIESG------PHCANTE--IIVKLSDGRE---LC
CXCL9      TPVVRKGRCS--CISTNQGTIHLQSLKDLKQFAPS------PSCEKIE--IIATLKNGVQT---C
CXCL10     VPLSRTVRCT--CISISNQPVNPRSLEKLEIIPAS------QFCPRVE--IIATMKKKGEKR--C
CXCL11     FPMFKRGRCL--CIGPGVKAVKVADIEKASIMYPS------NNCDKIE--VIITLKENKGQR--C
p1754        YIPIYVCM--CIH-SYALYNSILVSDGLRMLR---------CSHK---IIISTLTITF---LC
p0711     LIFPAIHSLCL--CDSGRIPARNALDPSQDQQPLQQDKDGTETMCVAGSNLNVHSWVNEERK---C
p2882     QFYMNFESVCR--CLQKISVIL-IGIAFNLCNDLGSIVILTV-LCILIHEYEIYFLLFRSLIFSLC
p0210      FQRSHMDYCDE-CTLQGVFPEHRSNQRAAREVLPTP-----KHCRLIPLGTVLSECPFQAP---C
p4922         GHAQPCFLICFQQHLPPTPLGSLKGPKID----------LCIHGTPPTCLSAQC------LC
                   §   §                                §                    §
```

C-terminal region

```
CXCL1                    LNPASPIVKKIIEKMLNSDKSN
CXCL2                    LNPASPMVKKIIEKMLKNGKSN
CXCL3                    LNPASPMVQKIIEKILNKGSTN
CXCL4                    LDLQAPLYKKIIKKLLES
CXCL5                    LDPEAPFLKKVIQKILDGGNKEN
CXCL6                    LDPEAPFLKKVIQKILDSGNKKN
CXCL7                    LDPDAPRIKKIVQKKLAGDESAD
CXCL8                    LDPKENWVQRVVEKFLKRAENS
CXCL9                    LNPDSADVKELIKKWEKQVSQKKKQKNGKKHQKKKVLKVRKSQRSRQKKTT
CXCL10                   LNPESKAIKNLLKAVSKERSKRSP
CXCL11                   LNPKSKQARLIIKKVERKNF
p1754                    LHAEILTNGLQLPTVFSTPACCTGW
p0711                  GISIQCNIIQPLQSRKLCRLLQQR
p2882                    FIVPEYSKFCNFYVKFILKNLFLMLS
p0210           WPQTKAIILNLWRNLEVLEVDRSLRQDCFKCTILLEFF
p4922             WDRQQVLKSQPLLPAGVHLRTFPAI
```

Figure 10

N- Terminal Region

```
CCL1    MQIITTALVCLLLAGMWPEDVDSKSMQV
CCL2    MKVSAALLCLLLIAATFIPQGLAQPDAIN
CCL3    MQVSTAALAVLLCTMALCNQFSASLAAD
CCL4    MKLCVTVLSLLMLVAAFCSPALSAPMGSD
CCL5    MKVSAAALAVILIATALCAPASASPYSS
CCL7    MKASAALLCLLLTAAAFSPQGLAQPVGIN
CCL8    MKVSAALLCLLLMAATFSPQGLAQPDSVS
p4711   MVTPIWTLFICYCLTSLLVLQAIFKEIDNILSEVDLNQ
p4320   MLFTLLFRILIGYVRTLW
p5008   MIFGLLIKALYLASAWAGALSLGAAGIWG
```

Cys-rich region

```
CCL1    PFSRCCFSFAEQEIPLRAILCYRN-TSSI-------------CSNEGLIFKLKRGKEA-CALD
CCL2    APVTCCYNFTNRKISVQRLASYRRITSSK-------------CPKEAVIFKTIVAKEI-CAD
CCL3    TPTACCFSYTSRQIPQNFIADYFE-TSSQ-------------CSKPGVIFLTKRSRQV-CAD
CCL4    PPTACCFSYTARKLPRNFVVDYYE-TSSL-------------CSQPAVVFQTKRSKQV-CAD
CCL5    DTTPCCFAYIARPLPRAHIKEYFY-TSGK-------------CSNPAVVFVTRKNRQV-CAN
CCL7    TSTTCCYRFINKKIPKQRLESYRRTTSSH-------------CPREAVIFKTKLDKEI-CAD
CCL8    IPITCCFNVINRKIPIQRLESYTRITNIQ-------------CPKEAVIFKTKRGKEV-CAD
p4711   HPVRCCYSFPTFCVEGMLLKLCFNMEPH-------------CFLSLTQSTVSLSQG--CHL
p4320   TKNSCCCWRMILNHSFKQEVPMIVELKQK----------CEMFCQKYLVDKDYSFRVSVTCQFF
p5008   WMTLCCGCCPVHYRTLRSIPDHNLLDASSTPSLVMTTRNISRHCQCPLVAKSSPAENE--CCTV
            §§                                          §                 §
```

C-terminal region

```
CCL1              TVGWVQRHRKMLRHCPSKRK
CCL2            PKQKWVQDSMDHLDKQTQTPKT
CCL3            PSEEWVQKYVSDLELSA
CCL4            PSESWVQEYVYDLELN
CCL5            PEKKWVREYINSLEMS
CCL7            PTQKWVQDFMKHLDKKTQTPKL
CCL8            PKERWVRDSMKHLDQIFQNLKP
p4711             FSVFVQLIWTAHLDRHKE
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p5008           IPPFQINRALRNECFLLLLSL
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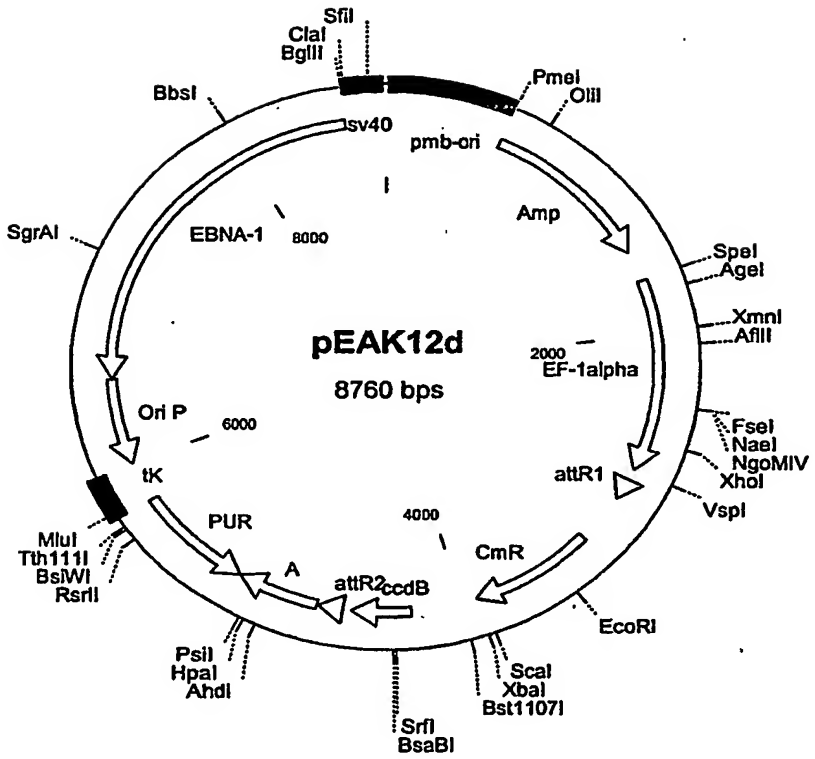
Figure 11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AflII
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Ori P
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FseI
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NgoMIV
XhoI
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PUR
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tag
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Val Ser Asp Gly Leu Arg Met Leu Arg Cys Ser His Lys Ile Ile Ile
50 55 60

Ser Thr Leu Thr Ile Thr Phe Leu Cys Leu His Ala Glu Ile Leu Thr
65 70 75 80

Asn Gly Leu Gln Leu Pro Thr Val Phe Ser Thr Pro Ala Cys Cys Thr
85 90 95

Gly Trp

<210> 3
<211> 336
<212> DNA
<213> Homo sapiens

<400> 3
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aaaaatagtg tatttcattt aattttcccc gctattcaca gtttatgctt atgtgattct
120

ggaagaattc cagctaggaa tgccttggac ccatcccagg accagcaacc cctgcagcag
180

gacaaagatg gcactgagac tatgtgtgta gctggaagca acctaaatgt ccattcgtgg
240

gtgaatgaag aaagaaaatg tggcatatcc atacaatgta atatcattca gcctttacaa
300

agtaggaaac tctgccgttt gctgcaacag agatga
336

<210> 4
<211> 109
<212> PRT
<213> Homo sapiens

<400> 4

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Met Val Ile Pro His Leu Val Leu Leu Thr Leu Ile Ser Phe Arg Leu
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Lys Glu Lys Asn Ser Val Phe His Leu Ile Phe Pro Ala Ile His Ser
            20                  25                  30

Leu Cys Leu Cys Asp Ser Gly Arg Ile Pro Ala Arg Asn Ala Leu Asp
        35                  40                  45

Pro Ser Gln Asp Gln Gln Pro Leu Gln Gln Asp Lys Asp Gly Thr Glu
    50                  55                  60

Thr Met Cys Val Ala Gly Ser Asn Leu Asn Val His Ser Trp Val Asn
65                  70                  75                  80

Glu Glu Arg Lys Cys Gly Ile Ser Ile Gln Cys Asn Ile Ile Gln Pro
                85                  90                  95

Leu Gln Ser Arg Lys Leu Cys Arg Leu Leu Gln Gln Arg
            100                 105
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<210> 5
<211> 330
<212> DNA
<213> Homo sapiens

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ctgcaattct atatgaattt cgaatcagtt tgtcgatgtc tgcaaaaaat ctctgtgatt
120

ctgataggga ttgcttttaa cctgtgtaac gatttgggga gtattgtcat tttaacagtg
180

ttatgtattc taatccatga atatgaaata tatttccttt tgtttagatc tttgattttt
240

tcattatgtt ttatagttcc agagtatagt aagttttgca atttttatgt taaatttatt
300

cttaagaatt tatttttgat gctatcataa
330

<210> 6

<211> 107
<212> PRT
<213> Homo sapiens

<400> 6

Met Ser Pro Ser Leu Phe Phe Ile Phe Lys Ile Val Leu Ala Ile Val
1 5 10 15

Asp Ser Leu Gln Phe Tyr Met Asn Phe Glu Ser Val Cys Arg Cys Leu
20 25 30

Gln Lys Ile Ser Val Ile Leu Ile Gly Ile Ala Phe Asn Leu Cys Asn
35 40 45

Asp Leu Gly Ser Ile Val Ile Leu Thr Val Leu Cys Ile Leu Ile His
50 55 60

Glu Tyr Glu Ile Tyr Phe Leu Leu Phe Arg Ser Leu Ile Phe Ser Leu
65 70 75 80

Cys Phe Ile Val Pro Glu Tyr Ser Lys Phe Cys Asn Phe Tyr Val Lys
85 90 95

Phe Ile Leu Lys Asn Leu Phe Leu Met Leu Ser
100 105

<210> 7
<211> 315
<212> DNA
<213> Homo sapiens

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gtattacagg ctatatttaa agaaatagat aacattctct ctgaggttga tttaaaccaa
120

catcctgtac gttgctgcta tagcttccca acattttgtg tagaggggat gctattgaag
180

ttgtgtttta atatggagcc acactgtttt ctttctctga cccagtctac agtcagcctg
240

tcccaaggct gccatctatt ctctgtgttt gtgcagctca tctggacagc tcatctggac
300

agacacaaag aatag
315

<210> 8
<211> 102
<212> PRT
<213> Homo sapiens

<400> 8

Met Val Thr Pro Ile Trp Thr Leu Phe Ile Cys Tyr Cys Leu Thr Ser
1 5 10 15

Leu Leu Val Leu Gln Ala Ile Phe Lys Glu Ile Asp Asn Ile Leu Ser
20 25 30

Glu Val Asp Leu Asn Gln His Pro Val Arg Cys Cys Tyr Ser Phe Pro
35 40 45

Thr Phe Cys Val Glu Gly Met Leu Leu Lys Leu Cys Phe Asn Met Glu
50 55 60

Pro His Cys Phe Leu Ser Leu Thr Gln Ser Thr Val Ser Leu Ser Gln
65 70 75 80

Gly Cys His Leu Phe Ser Val Phe Val Gln Leu Ile Trp Thr Ala His
85 90 95

Leu Asp Arg His Lys Glu
100

<210> 9
<211> 312
<212> DNA
<213> Homo sapiens

<400> 9
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acgaaaaatt cttgctgctg ttggcgaatg attttaaatc attcatttaa acaagaagtg
120

cctatgattg tagagctaaa gcaaaaatgt gaaatgtttt gtcagaaata tctagttgat
180

aaagattatt cctttcgtgt ttctgtaacc tgtcagttct ttatactttt acatgattcc

240

tacccaactg agaatacatg gtcaactatt ccaacattgt ctgctcttat atcctctttg
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atttttctgt ga
312

<210> 10
<211> 101
<212> PRT
<213> Homo sapiens

<400> 10

Met Leu Phe Thr Leu Leu Phe Arg Ile Leu Ile Gly Tyr Val Arg Thr
1 5 10 15

Leu Trp Thr Lys Asn Ser Cys Cys Cys Trp Arg Met Ile Leu Asn His
20 25 30

Ser Phe Lys Gln Glu Val Pro Met Ile Val Glu Leu Lys Gln Lys Cys
35 40 45

Glu Met Phe Cys Gln Lys Tyr Leu Val Asp Lys Asp Tyr Ser Phe Arg
50 55 60

Val Ser Val Thr Cys Gln Phe Phe Ile Leu Leu His Asp Ser Tyr Pro
65 70 75 80

Thr Glu Asn Thr Trp Ser Thr Ile Pro Thr Leu Ser Ala Leu Ile Ser
85 90 95

Ser Leu Ile Phe Leu
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<210> 11
<211> 345
<212> DNA
<213> Homo sapiens

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gctctgagcc tcggcgctgc tggcatttgg ggctggatga ctctttgctg tggctgctgt
120

cctgtgcatt acaggacatt acgtagcatc cctgaccaca acctactaga tgccagtagc
180

acccccctccc tagttatgac aaccagaaac atctccagac attgccaatg tcccctggtg
240

gcaaaatcat ccccggctga gaatgagtgt tgcacggtaa ttcctccatt ccaaattaac
300

agagcactta ggaacgagtg ctttctccta ttactttccc tttaa
345

<210> 12
<211> 112
<212> PRT
<213> Homo sapiens

<400> 12

Met Ile Phe Gly Leu Leu Ile Lys Ala Leu Tyr Leu Ala Ser Ala Trp
1 5 10 15

Ala Gly Ala Leu Ser Leu Gly Ala Ala Gly Ile Trp Gly Trp Met Thr
20 25 30

Leu Cys Cys Gly Cys Cys Pro Val His Tyr Arg Thr Leu Arg Ser Ile
35 40 45

Pro Asp His Asn Leu Leu Asp Ala Ser Ser Thr Pro Ser Leu Val Met
50 55 60

Thr Thr Arg Asn Ile Ser Arg His Cys Gln Cys Pro Leu Val Ala Lys
65 70 75 80

Ser Ser Pro Ala Glu Asn Glu Cys Cys Thr Val Ile Pro Pro Phe Gln
85 90 95

Ile Asn Arg Ala Leu Arg Asn Glu Cys Phe Leu Leu Leu Leu Ser Leu
100 105 110

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13

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tccagatttc aactaaaact cttgtttcac tgttttcaag gacttttcca aaggtcacac
120

atggactatt gtgatgaatg cactctgcag ggtgtgttcc cagagcacag aagtaaccag
180

agagctgcaa gggaggtgtt gcccacacca aaacactgca gacttattcc cctggggaca
240

gtgctgtcag agtgtccatt tcaagctccc tgttggccac agacaaaagc cattatccta
300

aatctctggc gaaacttgga ggtcttagaa gtggacagaa gtttaagaca ggattgcttt
360

aaatgcacaa ttttgttaga atttttctga
390

<210> 14
<211> 127
<212> PRT
<213> Homo sapiens

<400> 14

Met Gly Phe Val Val Leu Cys Leu Ile Phe Phe Leu Cys Lys Thr Gly
1 5 10 15

Met Asp Ser Arg Phe Gln Leu Lys Leu Leu Phe His Cys Phe Gln Gly
20 25 30

Leu Phe Gln Arg Ser His Met Asp Tyr Cys Asp Glu Cys Thr Leu Gln
35 40 45

Gly Val Phe Pro Glu His Arg Ser Asn Gln Arg Ala Ala Arg Glu Val
50 55 60

Leu Pro Thr Pro Lys His Cys Arg Leu Ile Pro Leu Gly Thr Val Leu
65 70 75 80

Ser Glu Cys Pro Phe Gln Ala Pro Cys Trp Pro Gln Thr Lys Ala Ile
85 90 95

Ile Leu Asn Leu Trp Arg Asn Leu Glu Val Leu Glu Val Asp Arg Ser

100 105 110

Leu Arg Gln Asp Cys Phe Lys Cys Thr Ile Leu Leu Glu Phe Phe
115 120 125

<210> 15
<211> 282
<212> DNA
<213> Homo sapiens

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gcagcagggc acgcacagcc ctgttttctc atctgctttc agcagcattt gcctcctact
120

ccacttgggt cactcaaggg tcccaaaata gacctgtgca ttcatgggac ccctcccacc
180

tgcctctctg ctcagtgtct ctgttgggac aggcagcaag tgcttaaatc ccagccactg
240

ctccccgctg gagtccacct gagaactttc ccagcaattt ga
282

<210> 16
<211> 91
<212> PRT
<213> Homo sapiens

<400> 16

Met Met Arg Val Leu Arg Leu Leu Ala Arg Val Leu Leu Gly Gln Leu
1 5 10 15

Leu Leu Ala Ala Gly His Ala Gln Pro Cys Phe Leu Ile Cys Phe Gln
20 25 30

Gln His Leu Pro Pro Thr Pro Leu Gly Ser Leu Lys Gly Pro Lys Ile
35 40 45

Asp Leu Cys Ile His Gly Thr Pro Pro Thr Cys Leu Ser Ala Gln Cys
50 55 60

Leu Cys Trp Asp Arg Gln Gln Val Leu Lys Ser Gln Pro Leu Leu Pro
65 70 75 80

Ala Gly Val His Leu Arg Thr Phe Pro Ala Ile
85 90

<210> 17
<211> 21
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<213> synthetic construct

<400> 17
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<210> 18
<211> 20
<212> DNA
<213> synthetic construct

<400> 18
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<210> 19
<211> 25
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<400> 19
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<210> 20
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<400> 20
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25

<210> 21
<211> 22
<212> DNA
<213> synthetic construct

<400> 21
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22

<210> 22
<211> 20
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<213> synthetic construct

<400> 22
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<210> 23
<211> 22
<212> DNA
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<400> 23
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22

<210> 24
<211> 23
<212> DNA
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<400> 24
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23

<210> 25
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<400> 25
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<210> 26
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<212> DNA
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<400> 26
tcatctctgt tgcagcaaac g
21

<210> 27
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<400> 27
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<210> 28
<211> 20
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<400> 28
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<210> 29
<211> 37
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<400> 29
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<210> 30
<211> 32
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<400> 30
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32

<210> 31
<211> 42
<212> DNA
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<400> 31
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42

<210> 32
<211> 37
<212> DNA
<213> synthetic construct

<400> 32
gtgatggtga tggtgaattg ctgggaaagt tctcagg
37

<210> 33
<211> 39
<212> DNA
<213> synthetic construct

<400> 33
aagcaggctt cgccacccat gatctttggc ctgctaatc
39

<210> 34
<211> 33
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<400> 34
gtgatggtga tggtgaaggg aaagtaatag gag
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<210> 35
<211> 39
<212> DNA
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<400> 35
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<210> 36
<211> 35
<212> DNA
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<400> 36
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<210> 37
<211> 36
<212> DNA
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<400> 37
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<210> 38
<211> 33
<212> DNA
<213> synthetic construct

<400> 38
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<210> 39
<211> 38
<212> DNA
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<400> 39
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<210> 40
<211> 32
<212> DNA
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<400> 40

gtgatggtga tggtgcagaa aaatcaaaga gg
32

<210> 41
<211> 57
<212> DNA
<213> synthetic construct

<400> 41
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57

<210> 42
<211> 68
<212> DNA
<213> synthetic construct

<400> 42
ggggaccact ttgtacaaga aagctgggtt tcaatggtga tggtgatggt gccaacctgt
60

acagcatg
68

<210> 43
<211> 62
<212> DNA
<213> synthetic construct

<400> 43
ggggacaagt ttgtacaaaa aagcaggctt cgccaccctg actatgatga gggtgctaag
60

gc
62

<210> 44
<211> 73
<212> DNA
<213> synthetic construct

<400> 44
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gaaagttctc agg
73

<210> 45
<211> 59
<212> DNA
<213> synthetic construct

<400> 45
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59

<210> 46
<211> 69
<212> DNA
<213> synthetic construct

<400> 46
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taataggag
69

<210> 47
<211> 59
<212> DNA
<213> synthetic construct

<400> 47
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59

<210> 48
<211> 71
<212> DNA
<213> synthetic construct

<400> 48
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60

taacaaaatt g

71

<210> 49
<211> 56
<212> DNA
<213> synthetic construct

<400> 49
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56

<210> 50
<211> 69
<212> DNA
<213> synthetic construct

<400> 50
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cagcaaacg
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<210> 51
<211> 58
<212> DNA
<213> synthetic construct

<400> 51
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58

<210> 52
<211> 68
<212> DNA
<213> synthetic construct

<400> 52
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caaagagg
68